

APPLICANT: MAO, JOYCE
TITLE OF INVENTION: CDNA CLONE HAP0167 THAT ENCODES
TITLE OF INVENTION: A HUMAN 7-TRANSMEMBRANE RECEPTOR
NUMBER OF SEQUENCES: 4
CORRESPONDENCE ADDRESS:
ADDRESSEE: RATNER & PRESTIA
STREET: P.O. BOX 980
CITY: VALLEY FORGE
STATE: PA
COUNTRY: USA
ZIP: 19482
COMPUTER READABLE FORM:
MEDIUM TYPE: Diskette
COMPUTER: IBM Compatible
OPERATING SYSTEM: DOS
SOFTWARE: Fastseq for Windows Version 2.0
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/08/956,322
FILING DATE: 23-OCT-1997
CLASSIFICATION: 536
PRIOR APPLICATION DATA:
APPLICATION NUMBER: 60/049,329
FILING DATE: 11-JUN-1997
ATTORNEY/AGENT INFORMATION:
NAME: PRESTIA, PAUL F
REGISTRATION NUMBER: 23,031
REFERENCE/DOCKET NUMBER: GH-70075
TELECOMMUNICATION INFORMATION:
TELEPHONE: 610-407-0700
TELEFAX: 610-407-0701
TELEX: 846169
INFORMATION FOR SEQ ID NO: 2:
SEQUENCE CHARACTERISTICS:
LENGTH: 652 amino acids
TYPE: amino acid
STRANDEDNESS: single
TOPOLOGY: linear
MOLECULE TYPE: protein
US-08-956-322-2

Query Match 17.0%; Score 776; DB 4; Length 652;
Best Local Similarity 33.6%; Pred. No. 1,8e-61;

Matches 184; Conservative 102; Mismatches 229; Indels 32; Gaps 11;

QY 35 TPGKDSAASTSLNKAMETVNNLLQPOLNAMRDLTSDQLRAATMLHTHYEESAFVLAD 94
DB 120 TTSSKTQGGKELQKIDKRESLITNQL--WRREGQELSSYRTTILRDVESVLETL 177
QY 95 NLKTDIVRENTDNKLEVARLSTEGNLEDKPEPNMGHSTIOLSANILKONGRGEIR 154
DB 178 KDEQKVLKIONDSVAIETQITDNCSEERKTFULNVQUNS-MDIRCSDIQGTQGPSA 236
QY 155 VAFVLYNNGRPYLSTENASKKLGTALSTHNSVYVNSPVYTAATNFKSNKYIADYVF 214
DB 237 IATLISLISLNI--NATF--FEENDKQDYLYNSQVSAALGPR--RNVSLSKSVTL 288
QY 215 TVRHINQSEENFNPNCSFMSYSKRTMTG-YWSTQGCRLTNTKTHTCSCNHLTFNFAVL 273
DB 289 TPOHVKMTPESTKKECYVM--KSTGGSGMSRQGCFLIHVNSHTKCNKSHLSFPAVL 345
QY 274 AHVEVKHSDAVHDLIDVTWVGILSLVCLICITFCFGRGLOSDRNTIHKMLCISLF 333
DB 346 ALTSQE-----EDPVLIVITVYVGLSVSLCLLALLFLCKALQONSTSLHQLSLCLF 400
QY 334 VALLEFLIGINTDQIPACAVFAALLHFFLAFTWFLGVOLYT---MLVEVFSEH 389
DB 401 LAHLFLVGLIDREPKVLCIIAGALHYLYLAFTWMLGVLHFLARMLTYVNVSSIN 460
QY 390 SRRKY-FYLVGYGMPALIVSAADVRSYGTQVCWLRDLTYFIMSGPATILIMLVN 448
DB 461 RLKWMIFPVGYVPATVVAISASMPHLGYTDRCWLHLDGGWMSFLGVCATFSAVL 520
QY 449 IFGLIALYKMFHHTALIKPESGCLDNKISWVGAIALLLGLITWAGLMIYNESVIMA 508

DB 521 VLFILVFWILKRKLSINSEVSTIQNTNMLAFKRTAQLFLLIGTCWGLLOVGPAAVMA 580
QY 509 YLFTFNSLQGMFTFTHCVLQKKVREYKGLCLRTHCCSGKSTSSIGSK-----TS 561
DB 581 YLFTFINSLOGFLEFLVYLCILSDQVOKOYOKWFEIRVKSSESETYLLSKMGPDSK 640
QY 562 GSRTGGR 568
DB 641 GDVPRGQ 647

RESULT 3

US-09-284-819-6
Sequence 6, Application US/09284819
Patent No. 6365712

GENERAL INFORMATION:

APPLICANT: Kelly, Kathleen

APPLICANT: The Government of the United States of America

APPLICANT: as represented by The Secretary of the

APPLICANT: Department of Health and Human Services

TITLE OF INVENTION: Methods and Compositions for Inhibiting Inflammation

TITLE OF INVENTION: and Angiogenesis Comprising a Mammalian CD97 Alpha

FILE REFERENCE: Subunit

CURRENT APPLICATION NUMBER: US/09/284, 819

CURRENT FILING DATE: 1999-08-20

EARLIER APPLICATION NUMBER: US 60/027, 871

EARLIER FILING DATE: 1996-10-25

EARLIER APPLICATION NUMBER: WO PCT/US97/19772

EARLIER FILING DATE: 1997-10-24

NUMBER OF SEQ ID NOS: 21

SOFTWARE: PatentIn Ver. 2.1

SEQ ID NO 6

LENGTH: 835

TYPE: PRT

ORGANISM: Homo sapiens

FEATURE:

OTHER INFORMATION: CD97amino acid sequence encoded by full-length

US-09-284-819-6

Query Match 17.0%; Score 775; DB 4; Length 835;
Best Local Similarity 33.3%; Pred. No. 3,4e-61;

Matches 191; Conservative 108; Mismatches 211; Indels 64; Gaps 18;

QY 30 QLRNLTPGCGDSAASTSLNKAMETVNNLLQPOLNAMRDLTSDQLRAATMLHTHYEES 88
DB 281 KYVDLGRDSKSTSAEVTIQNVIKLVDELMEAPGDVEA--LAPVRRLITQLLSNLEID 337
QY 89 AFVLAIDLKTDIVRENTDNKLEVARLSTEGNLEDKPEPNMGH-STIOLSANILKON 147
DB 338 MRIAKSLPRGPFYIYSPSTELTL-MIOERGD-----KNYMGSSAKMKLMAVAA 389
QY 148 GRN--GEIRVAFVLYNNGRPYLSTENASKKLGTALSTHNSVYVNSPVY-----TAAT 198
DB 390 GAEDPGAVAGIISIQMTLLA--NASLNIHSHKQKLEIYEISS--INGVOLRLSLAV 445
QY 199 NKEF---SKNYIADPVYFVYKHKQSE-----ENNNPN-----CSFMSYSKRTM 240
DB 446 NSIFLSHNNTKELNSPLTFAPFSLHSSSDGAGRDPAPKADWPGRRDQLCAFWK-SDSDR 504
QY 241 TGWSTQGCRLTNTKTHTCSCNHLTFNFAVMAHVEVKHSDAVHDLIDVTWVGILSL 300
DB 505 GGHNAIEGCOVLSKNGKSTICQCSHLSFALMAHVE-----DKKLTLIRVGLALS 558
QY 301 LVCLLICITFCFGRGLOSDRNTIHKMLCISLFAELLFLIGINTDQIPACAVFAAL 358
DB 559 LFCLLCITLFLVLRPIQSGRTIHLHLCLCFVGSITFLAGIENEGGVGLGRLVAGL 618
QY 359 LHFFFLAFTWMLGVOLYTLMVEVFESHSRRKYFYLVGYGMPALIVSAADVRSY 418
DB 619 LHVCFLAAPCMMSLDEGLYFLVVRVPOGGLSTRMLCLIGYGVPLIVGVSAIYSGY 678

Db 173 CVM--KSTGGSQNSRDCFLIHNKSHMCNCSHLSFAVIALMTSGE-----BDPV 224
QY 289 LDVITWVGLLSLVCLLICTFPCFFRGLOSDRNTIHNKLSIFVALLFGLIGINTDQ 348
Db 225 LVITVGLSVSLCLLALLFLCKAIQNTSLSHLQSLCFLAHLFLVIGIDTTP 284
QY 349 PIACAFALLHFFFLAFTWFLFEGVQLYT---MLVEFESEHSRRKY-FYLVGMP 403
Db 285 KVICSTIAGLHLYLAFTWMLFEGHFLFARNLTVVVSSINRLMKIMFPGVGP 344
QY 404 ALIYAASAVDYRSYGDKCMRLDTYFIMSFIPATLIMLVNIFGLYALYKMFHTA 463
Db 345 AVVAISAASMPHLXGADKCMHLDGFMWSEGLPVCAIFSANLVFLIVFLKRLS 404
QY 464 ILKPESGCLDNKSWIGALIALCLGLTWAFLMYINESTVIMAYLFTFNSLOGMFI 523
Db 405 SLNSESTIQNTRLAFKATQFLIGCTWCLGLQVPAQVAYLFTIINSLOGFEIF 464
QY 524 IFHCVLQKRYKREYKCLRTHCSSGKSTESSISGK-----TSGSRTPGR 568
Db 465 LVYCLLSQOVQYQKWFREIVKSKSESTYTLSSKMKPDSKPEGDVFPQ 516

RESULT 6

US-09-110-116-3
; Sequence 3, Application US/09110116
; Patent No. 6013479
; GENERAL INFORMATION:
; APPLICANT: Xu, Hong
; APPLICANT: Cohen, Victoria L.
; TITLE OF INVENTION: HUMAN EMRI-LIKE G PROTEIN COUPLED
; FILE REFERENCE: PF-0550 US
; CURRENT APPLICATION NUMBER: US/09/110,116
; CURRENT FILING DATE: 1998-07-02
; NUMBER OF SEQ ID NOS: 4
; SOFTWARE: FastSeq for Windows Version 3.0
; SEQ ID NO 3
; LENGTH: 886
; TYPE: PRP
; ORGANISM: HOMO SAPIENS
; FEATURE:
; OTHER INFORMATION: 784994, GenBank
US-09-110-116-3

Query Match 15.7%; Score 715.5; DB 3; Length 886;

Best Local Similarity 30.4%; Pred. No. 9.5e-56;
Matches 166; Conservative 116; Mismatches 211; Indels 53; Gaps 12;

QY 47 NKAIVETVNNILQP-----QALNAMDLTTSQDLRAATMLHTVEESAFLAD---NL 97
Db 366 KTIIVTSLKNTTESFVPLKQISMWTFKTEKETSALATVLESE--SMLASFWKRSAN 423
QY 98 KTIIVRENTDNILEARLSTEGNLEDKPEENHGSGTQLSANTLKONGEIRVAF 157
Db 424 VTPAVR--AEYLDIESKVKKESEENVTL-DVAKGDKMKICSTIESESTETTVAF 480
QY 158 VLNNNGPSTENASMKLTETALSTHSIVNSPVITAINKEFSKVV-----207
Db 481 VSVVGHESVYN-----ERPDH---QAPLTSIKLKMNSRVVVGIMTEGKD 526
QY 208 -LADPVVFTKHKOSEENPNPCSEWSYKRTMTGYWSTOGCRLLTNKTHHTSCNHL 266
Db 527 GFDPITITLENVQPKOPKFRPTCVSWSTVYK--GGRWTFGCVILLEASSTYITCSNOM 584
QY 267 TNPAVLAHVEVKAHSDAHDLLDVTWVGLISLVCLLICTFPCFFRGLOSDRNTIK 326
Db 585 ANLAIVMASGEL-----TMDPSLIYISHVGIISIVCLVLAIAFTFLCRSIRHNHTYHL 639
QY 327 NLCISLFAVELLFLIGINTDQPIACAVFAALLHFFFLAFTWFLFEGVQLYT---L 381
Db 640 HLCVCLLAKTLFLAGIHKTKNGCATIAGFLHYLFLACFEMVLVEAVILFLVNRKV 699

QY 382 VEVFESEHSRRKYFYLVGYMPALIVAASAVDYRSYGDKVCMLRDTYFIMSFIPAT 441
Db 700 VNFESSNIMLMHICARGYGLPMLVVIVISASVQDGGMHNRCLNTEGFIINSFLCPVC 759
QY 442 LIIMLVNIFGLIALYKFFHHTALIKPESGCLDNKSWIGALIALCLGLTWAFLMYIN 501
Db 760 TVIVINSLTLTWMLIRORLSSVNAEVSPLKDTRLTFKFAFQFLIGCSWVLGFIQ 819
QY 502 ESTVIMAYLFTFINSLOGMFIIFHCVLQKRYKREYKCL--RTHCCSGKSTESSISGK 559
Db 820 PVAGVAYLFTIINSLOGAFIFLHCLLNQVDEYKRWITGKTPSSQSOTSRILSSM 879
QY 560 TSGSRT 565
Db 880 PSASKT 885

RESULT 7

US-09-110-116-4
; Sequence 4, Application US/09110116
; Patent No. 6013479
; GENERAL INFORMATION:
; APPLICANT: Xu, Hong
; APPLICANT: Cohen, Victoria L.
; TITLE OF INVENTION: HUMAN EMRI-LIKE G PROTEIN COUPLED
; FILE REFERENCE: PF-0550 US
; CURRENT APPLICATION NUMBER: US/09/110,116
; CURRENT FILING DATE: 1998-07-02
; NUMBER OF SEQ ID NOS: 4
; SOFTWARE: FastSeq for Windows Version 3.0
; SEQ ID NO 4
; LENGTH: 344
; TYPE: PRP
; ORGANISM: HOMO SAPIENS
; FEATURE:
; OTHER INFORMATION: 2935597, GenBank
US-09-110-116-4

Query Match 14.3%; Score 652.5; DB 3; Length 344;

Best Local Similarity 38.9%; Pred. No. 9.8e-51;
Matches 135; Conservative 67; Mismatches 126; Indels 19; Gaps 6;

QY 230 CSFMSYKRTMTGYWSTOGCRLLTNKTHHTGSCNHLTNPAVLAHVEVKAHSDAHDLL 289
Db 4 CVMWEHQNG-CGHWAITGCGTIGTRDTSTICRTHLSFAVIALMAHDVQ-----EDPV 57
QY 290 DVITWVGLLSLVCLLICTFPCFFRGLOSDRNTIHNKLSIFVALLFGLIGINTDQ 349
Db 58 TVITWGLSVSLCLLALLFLCKAIQNTSLSHLQSLCFLAHLFLVIGIDTTP 117
QY 350 IACAVFALLHFFFLAFTWFLFEGVQLYT---LVEFESEHSR--RKIFYLVGMPA 404
Db 118 VICSITAGLHLYLAFTWMLLEALYFLFARNLTVVVSSINREKMKIMFPGVGP 177
QY 405 LIYAASAVDYRSYGDKVCMLRDTYFIMSFIPATLIMLVNIFGLYALYKMFHTA 464
Db 178 VYVAISAASMPHLXGADKCMHLDGFMWSEGLPVCAIFSANLVFLIVFLKRLS 237
QY 465 ILKPESGCLDNKSWIGALIALCLGLTWAFLMYINESTVIMAYLFTFNSLOGMFI 524
Db 238 LNSEVSTLRNTRLAFKATQFLIGCTWCLGLQVPAQVAYLFTIINSLOGVFI 257
QY 525 FHCVLQKRYKREYKCL--RTHCCSGKSTESSISGKSTGSKRT 565
Db 298 VYCLLSQOVQYQKWSKGRKLKTE--SEMHTLSSAKADTSKPSR 342

RESULT 8

US-08-852-806-2
; Sequence 2, Application US/08852806


```

; Patent No. 5874245
; GENERAL INFORMATION:
; APPLICANT: Shoji Fukusumi
; APPLICANT: Shuji Hinuma
; TITLE OF INVENTION: NOVEL HUMAN G-PROTEIN COUPLED RECEPTOR
; NUMBER OF SEQUENCES: 14
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: SmithKline Beecham Corporation
; STREET: 709 Swedeland Road
; CITY: King of Prussia
; STATE: PA
; COUNTRY: U.S.A.
; ZIP: 19406-0939
; COMPUTER READABLE FORM:
; MEDIUM TYPE: Diskette
; COMPUTER: IBM Compatible
; OPERATING SYSTEM: DOS
; SOFTWARE: FASTSEQ Version 1.5
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/08/852,806
; FILING DATE:
; CLASSIFICATION: 435
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: 60/017,915
; FILING DATE: 16 MAY 1996
; ATTORNEY/AGENT INFORMATION:
; NAME: Han, William T
; REGISTRATION NUMBER: 34,344
; REFERENCE/DOCKET NUMBER: TAK50002
; TELECOMMUNICATION INFORMATION:
; TELEPHONE: 610-270-5219
; TELEFAX: 610-270-5090
; TELEX:
; INFORMATION FOR SEQ ID NO: 2:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 1052 amino acids
; TYPE: amino acid
; TOPOLOGY: linear
; STRANDEDNESS: single
; MOLECULE TYPE: peptide
; HYPOTHEICAL: NO
; ANTI-SENSE: NO
; FRAGMENT TYPE: N-terminal
; ORIGINAL SOURCE:
; US-08-852-806-2

Query Match 11.4%; Score 521.5; DB 2; Length 1052;
Best Local Similarity 22.3%; Pred. No. 5,2e-38;
Matches 233; Conservative 142; Mismatches 346; Indels 323; Gaps 43;

QY 10 AGDITYSVAMQDLVGLLVOLRLNLT-----PGKDSARSLINKAMVETVNNLQDP 60
; : : : : : : : : : : : : : : : : : : : : : : : : : : : : : :
DB 133 SGLDLFV-----DI-LRNVTDFKRAITYPSADV-----QRFQVYSHVDA 175
; : : : : : : : : : : : : : : : : : : : : : : : : : : : : : :
QY 61 QALNARDLTTSQDLRAATM-LHFE-----ESAFVLADNLL-----97
; : : : : : : : : : : : : : : : : : : : : : : : : : : : : : :
DB 176 EKKERKMD---AQVSPGSHLRVYEDFIHLVGDAKAFQSSLYTIDNLVLSIQREPVS 232
; : : : : : : : : : : : : : : : : : : : : : : : : : : : : : :
QY 98 -----KTDIVRENTDNKL-EVARLSTEGNEDL-----KF 127
; : : : : : : : : : : : : : : : : : : : : : : : : : : : : : :
DB 233 AVSSDITFPMRGRGKMDVVRHSEDRFLPKFVLSLSPGKPAISGAAGSPGRGPGTV 292
; : : : : : : : : : : : : : : : : : : : : : : : : : : : : : :
QY 128 PENMGHGSTIOLSAANTLAKNGRNGELRVAFLVNLNIGPLSTENASMKLGTEALSTNH5V 187
; : : : : : : : : : : : : : : : : : : : : : : : : : : : : : :
DB 293 PRGPGSHQRLLPADP---DESSYFVIGAVLYRTLGLLPPRPPL-----335
; : : : : : : : : : : : : : : : : : : : : : : : : : : : : : :
QY 188 IYNSPITYAIINKEFSNKYVLADPVVETVKHIKOSENFNPNCSEFYSYKR-TMGWGS 246
; : : : : : : : : : : : : : : : : : : : : : : : : : : : : : :
DB 336 ATTSKMTYTVRPPYOP---AEPIL-YVELSTIITGTDPRKASADYSRADASSGDMPT 391
; : : : : : : : : : : : : : : : : : : : : : : : : : : : : : :
QY 247 QGCRLITTKTKHTTSCNHLINFAVLMAHVEVKSDAVDLLDVTWVGIILSLVCLLI 306
; : : : : : : : : : : : : : : : : : : : : : : : : : : : : : :
DB 392 ENCGTLETOAHTRCOCCHLSTFAVL-----AQPRLDTLELAGSPSVPLVICAVS 443

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QY 307 CIEFF-----CEFRGLOSDRNTIHKNICISLFVAELLFLIGINRTDQPIACVFAALL 359
; : : : : : : : : : : : : : : : : : : : : : : : : : : : : : :
DB 444 CMALLTLTLLAIYAFWRFPISESRITLLNPLCLSLASNNILLVQSVLSKGVCTMTAAFL 503
; : : : : : : : : : : : : : : : : : : : : : : : : : : : : : :
QY 360 HFFFLAFTMPLEGGVQLIMLEVFESESRKRYLYVGYGMPALIVASAA-VVYRSY 418
; : : : : : : : : : : : : : : : : : : : : : : : : : : : : : :
DB 504 HFFFLSPCWVLEAMQSLAVIGRMTRLYRRR-FLCLQWGLPALVAVSVGFTFTKCY 562
; : : : : : : : : : : : : : : : : : : : : : : : : : : : : : :
QY 419 GTDKVCLRLDYFTWSEFTGPAITLIMLVIFGLALYKMFHHTTALIKPESGLDNKSM 478
; : : : : : : : : : : : : : : : : : : : : : : : : : : : : : :
DB 563 GTSSYCMLEGGILYAFVGAIPAIVLVNML-IGIIVFNK-----LMARDGISDKRQ 615
; : : : : : : : : : : : : : : : : : : : : : : : : : : : : : :
QY 479 VIGA-----IALLCLGLTWARGMLYINE-STYIMAYLFTINSLOCMFTFHYCLQKK 532
; : : : : : : : : : : : : : : : : : : : : : : : : : : : : : :
DB 616 RAGASIMSSCVPLPLALMTMSAVLAMTBRSVLFQALRAVFNASAGFYTAHVCFRRR 675
; : : : : : : : : : : : : : : : : : : : : : : : : : : : : : :
QY 533 VRKEYGCLRTHCSCGSTSESSIGSGKTSRTPRGYSQSQRIRRMNDTVRKQSESS 592
; : : : : : : : : : : : : : : : : : : : : : : : : : : : : : :
DB 676 V-QDVVKCQMGVCRADESEDS-----PDSCKNGQLILSDFEKV-----714
; : : : : : : : : : : : : : : : : : : : : : : : : : : : : : :
QY 593 FITGDINSSASLNRGLNARDTSVMDLP-----LNGNHN-SYSTASGE 638
; : : : : : : : : : : : : : : : : : : : : : : : : : : : : : :
DB 715 ---DIACOTVLFKE--VNTCNPSTYTGTLRLSLDEDEPKSKCLVGPBGSLSFPLPGN 768
; : : : : : : : : : : : : : : : : : : : : : : : : : : : : : :
QY 639 YL-----SNCVQIIDRCYNHNETALEKKILKELTSNYTIPSYLNHNS 681
; : : : : : : : : : : : : : : : : : : : : : : : : : : : : : :
DB 769 ILVPMASPGELGPPPPQEPNPMYMGEGG-----LNQIDL--TWLRPTERG 813
; : : : : : : : : : : : : : : : : : : : : : : : : : : : : : :
QY 682 SEQNRMIMNKLYVNNLT-----GSGREDDATVLDAT-----SFNHESLGL 721
; : : : : : : : : : : : : : : : : : : : : : : : : : : : : : :
DB 814 SEGDYVVLPRRLTSLQPGGGGGGGEADAPRARPGCTRRRAKTYAHTEGYPSFLSVHSGIL 873
; : : : : : : : : : : : : : : : : : : : : : : : : : : : : : :
QY 722 EL-----IHESDAPLLPPRV-----Y 738
; : : : : : : : : : : : : : : : : : : : : : : : : : : : : : :
DB 874 GLGPAYSLQNPYGMTFPPPPPTPSARQVPEPERSRTMPRTVPGSTMKGSLERKRLY 933
; : : : : : : : : : : : : : : : : : : : : : : : : : : : : : :
QY 739 STENHQPHNYTRRIRIQDSESEFFPLTNHTPDLOSPIRDSLYTSMPL-----A 789
; : : : : : : : : : : : : : : : : : : : : : : : : : : : : : :
DB 934 SLDLFKVMYTRKR---HSELYHELNQKFFTFD-----RYRSQSTAKRKRKSVSS 981
; : : : : : : : : : : : : : : : : : : : : : : : : : : : : : :
QY 790 GVATRESVTSQTPEPPPAKCGDAEDVYKSMPLGSRNHHQHLHTYYOGRGSSDGFYV 849
; : : : : : : : : : : : : : : : : : : : : : : : : : : : : : :
DB 982 GGAERSVCTD---KSPGE-----RSLSQHRRHQSNTFKSMITLGS-----L 1022
; : : : : : : : : : : : : : : : : : : : : : : : : : : : : : :
QY 850 PPN-----KDTTPEG 860
; : : : : : : : : : : : : : : : : : : : : : : : : : : : : : :
DB 1023 PKPRERLTLHRAAMEPTEPPDG 1046
; : : : : : : : : : : : : : : : : : : : : : : : : : : : : : :

RESULT 9
US-09-163-669-2
; Sequence 2, Application US/09163669
; Patent No. 6111076
; GENERAL INFORMATION:
; APPLICANT: FUKUSUMI, SHOJI
; APPLICANT: HINUMA, SHUJI
; TITLE OF INVENTION: NOVEL HUMAN G-PROTEIN COUPLED
; TITLE OF INVENTION: RECEPTOR (HIBCD07)
; NUMBER OF SEQUENCES: 14
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: Ralner & Prestia
; STREET: P.O. Box 980
; CITY: Valley Forge
; STATE: PA
; COUNTRY: USA
; ZIP: 19482
; COMPUTER READABLE FORM:
; MEDIUM TYPE: Diskette
; COMPUTER: IBM Compatible
; OPERATING SYSTEM: DOS
; SOFTWARE: FASTSEQ for Windows Version 2.0

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Db 729 -HSPHLCPLPSGNSOG 744

RESULT 13

US-08-982-412-2

Sequence 2, Application US/08982412

Patent No. 5938729

GENERAL INFORMATION:

APPLICANT: SOPPET, DANIEL R

APPLICANT: LI, YI

APPLICANT: ROSEN, CRAIG A

APPLICANT: ROSEN, STEVEN M

TITLE OF INVENTION: HUMAN G-PROTEIN RECEPTOR

NUMBER OF SEQUENCES: 7

CORRESPONDENCE ADDRESS:

ADDRESSEE: HUMAN GENOME SCIENCES, INC.

STREET: 9410 KEY WEST AVENUE

CITY: ROCKVILLE,

STATE: MD

COUNTRY: US

ZIP: 20850

COMPUTER READABLE FORM:

MEDIUM TYPE: Floppy disk

COMPUTER: IBM PC compatible

OPERATING SYSTEM: PC-DOS/MS-DOS

SOFTWARE: Patentin Release #1.0, Version #1.30

CURRENT APPLICATION DATA:

APPLICATION NUMBER: US/08/982,412

FILING DATE:

CLASSIFICATION:

ATTORNEY/AGENT INFORMATION:

NAME: BROOKES, ANDERS A

REGISTRATION NUMBER: 36,373

REFERENCE/DOCKET NUMBER: PF181PCT2

TELEPHONE: (301) 309-8504

TELEFAX: (301) 309-8439

INFORMATION FOR SEQ ID NO: 2:

SEQUENCE CHARACTERISTICS:

LENGTH: 884 amino acids

TYPE: amino acid

TOPOLOGY: 1linear

MOLECULE TYPE: protein

US-08-982-412-2

Query Match 10.4%; Score 475; DB 2; length 884;

Best local Similarity 24.2%; Pred. No. 6,4e-34;

Matches 193; Conservative 106; Mismatches 306; Indels 192; Gaps 27;

QY 189 VNSPVITAI-NKESNRYVADPVVTVKIKQSEENFNPCSFWS-YSKRTMTGWS 245

Db 1 MNSPVVSAVAFHGRNFRGI-LESPISEFRR-LIQTNRSKATCYQMDPGLAEQHGVT 58

QY 246 TQCCRLITTKHTTSCNLTNFVAVMAVEYKHSDAVDL-LDYITVYGIILSLVCL 304

Db 59 ARCELVHRHSGHAKRCSTGTGGVLMDSPPRELEG-DLELLAVTHVVAVSAAL 116

QY 305 LICIFTECFRGLOSDNRTIHKNCISLFAVELLEFLIGINRTDOPIACAVFAALLHFFFL 364

Db 117 VLRAIILSLRSLSKSNRGHANVAALGVALLEFLIGIRTNQVCTAVAILIHFEL 176

QY 365 AAFTMFLEGVOLYIMLVEFESEHSRKYVLYGMPALLIYVSAVAVDYRSYGTDKVC 424

Db 177 STEAMLEFVQGLHLYRMQYVERNVDRGAMRFYHALGMGVPAVLGLAVGLDPEGVGNDFC 236

QY 425 WLRLDYFTSFTGPATLITMLNVIPIGIALYKMFHTTALIKPESGLDNIKSVT--G 481

Db 237 WISVHEPLVMSFGPVVLYVMN-----GTMFLAARTSCSTGOREAKTSALTLS 288

QY 482 AIALCLLGLTMAFGMYINESTVIMAYLFTFINSLOGMFTIFHCYLOKKVREY-GKC 540

Db 289 SFLLILLVSAWLPGLLAVNHSLIARHYLHAGCGLGGLAVLLFCVLLADARAMPAC 348

QY 541 LRTHCSS-----GKSTESSIGKTSGRTPGRYS 570

Db 349 LGRKAPEARAPAGLPGAYNNMTALFEESGLIRITLGASTVSSARS--GRTODDS 406

QY 571 TGSQSRIRRMNDTVKROSSSF-----ITDDINSSASLNR 606

Db 407 QRGRSYLRD--NVLVRGSAADHTDLSLOAHAGPTDLVDMFHRDAGADSDSDSLTEE 464

QY 607 EGLLN-----NARDTSVMDLP--LNGNHSYSIASGE-YLSN 642

Db 465 ERSLSITSSSEEDNGRTGRFQRLPCRAGOSERLTHPRKYDNDLSYPALGECEAP 524

QY 643 C-----VQIDRGYNHN-----ETAL-----EKKILK-ELTSNYIPS 673

Db 525 CALQTWGSEERRLGIDTSKDAANNQPPALVTSGETSLGRAOROKRILKNRLOYPLVPQ 584

QY 674 YLNNHRSSEQNRLNKLNNLGSGR-----EDDAIYLDATSFNHEESGLIHLH----- 725

Db 585 TRGAPELSMCRAATLGRVAPASGRIVAGGTGSLQSPASRSRREGQDLRLRQLSR 644

QY 726 ---EESDAPLPP--RYVSTE-----NHOPHYTRRRIPODSESFPPLLTNEH 769

Db 645 ERLEAPAPVLRPLSRGSGECMDAARGLEPKDRGSTLPRQPPRDPGAMAGREGSRD 704

QY 770 TEDLOSPHSDSLYTSMTETLAVATSESVTSTQTEPPACGDAEDYVYKMPNLGSRNH 829

Db 705 ALDIGAP-REWL-----STLPPRRTRDL----- 728

QY 830 VHQHTYYQLCRGSSDC 846

Db 729 -HSPHLCPLPSGNSOG 744

RESULT 14

US-08-110-286A-6

Sequence 6, Application US/08110286A

Patent No. 5728545

GENERAL INFORMATION:

APPLICANT: Perrin, Marilyn H.

APPLICANT: Chen, Ruoping

APPLICANT: Lewis, Kathy A.

APPLICANT: Vale Jr., Wylie W.

TITLE OF INVENTION: CLONING AND RECOMBINANT PRODUCTION OF

TITLE OF INVENTION: CRF RECEPTOR(S)

NUMBER OF SEQUENCES: 6

CORRESPONDENCE ADDRESS:

ADDRESSEE: Pretty, Schroeder, Brueggemann & Clark

STREET: 444 South Flower Street, Suite 2000

CITY: Los Angeles

STATE: CA

COUNTRY: USA

ZIP: 90071

COMPUTER READABLE FORM:

MEDIUM TYPE: Floppy disk

COMPUTER: IBM PC compatible

OPERATING SYSTEM: PC-DOS/MS-DOS

SOFTWARE: Patentin Release #1.0, Version #1.25

CURRENT APPLICATION DATA:

APPLICATION NUMBER: US/08/110, 286A

FILING DATE:

CLASSIFICATION: 435

PRIOR APPLICATION DATA:

APPLICATION NUMBER: US 08/079,320

FILING DATE: 18-JUN-1993

ATTORNEY/AGENT INFORMATION:

NAME: Reiter, Stephen E.

REGISTRATION NUMBER: 31,192

REFERENCE/DOCKET NUMBER: P41 9439

TELEPHONE: 619-546-4737

TELEFAX: 619-546-9392

INFORMATION FOR SEQ ID NO: 6:

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OM protein - protein search, using sw model

Run on: December 10, 2002, 11:09:29 ; Search time 27 Seconds

(without alignments)
3104.786 Million cell updates/sec

Title: US-09-744-226a-1

Perfect score: 4563

Sequence: 1 AEQTRNHLNAGDITYSVRAM.....KDGPPSSGKGAHLYTSL 872

Scoring table:

BLOSUM62

Gapop 10.0 , Gapext 0.5

Searched: 283224 seqs, 96134422 residues

Total number of hits satisfying chosen parameters: 283224

Minimum DB seq length: 0

Maximum DB seq length: 2000000000

Post-processing: Minimum Match 0%

Maximum Match 100%

Listing first 45 summaries

Database :

1: p1r1:*
2: p1r2:*
3: p1r3:*
4: p1r4:*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	Query Match	Length	DB ID	Description
1	4456	97.7	1503	2	T18389 latrophilin-3, spl
2	4456	97.7	1571	2	T18395 latrophilin-3, spl
3	4441.5	97.3	1512	2	T18392 latrophilin-3, spl
4	4441.5	97.3	1580	2	T18407 latrophilin-3, spl
5	4401.5	96.5	1459	2	T17186 CL3AA protein - ra
6	4401.5	96.5	1527	2	T17198 CL3BA protein - ra
7	4370	95.8	1550	2	T14327 alpha-latrotoxin r
8	3123.5	68.5	1273	2	T17188 CL3AC protein - ra
9	3123.5	68.5	1341	2	T17200 CL3BC protein - ra
10	3123	68.4	1230	2	T17187 CL3AB protein - ra
11	3123	68.4	1298	2	T17199 CL3BB protein - ra
12	3120.5	68.4	1274	2	T18391 latrophilin-3, spl
13	3120.5	68.4	1342	2	T18405 latrophilin-3, spl
14	3120	68.4	1231	2	T18390 latrophilin-3, spl
15	3120	68.4	1299	2	T18398 latrophilin-3, spl
16	3106	68.1	1283	2	T18394 latrophilin-3, spl
17	3106	68.1	1351	2	T18409 latrophilin-3, spl
18	3105.5	68.1	1240	2	T18393 latrophilin-3, spl
19	3105.5	68.1	1308	2	T18408 latrophilin-3, spl
20	2646.5	58.0	1341	2	T18301 latrophilin-2 (spl)
21	2646.5	58.0	1407	2	T18381 latrophilin-2 (spl)
22	2630	57.6	1354	2	T18375 latrophilin-2 (spl)
23	2630	57.6	1420	2	T18385 latrophilin-2 (spl)
24	2624	57.5	1356	2	T18367 latrophilin-2, spl
25	2624	57.5	1422	2	T18383 latrophilin-2, spl
26	2619	57.4	1384	2	T18366 latrophilin-2 (spl)
27	2619	57.4	1450	2	T18382 latrophilin-2 (spl)
28	2607.5	57.1	1369	2	T18379 latrophilin-2 (spl)
29	2607.5	57.1	1435	2	T18387 latrophilin-2 (spl)

30	2602.5	57.0	1397	2	T18377 latrophilin-2 (spl)
31	2602.5	57.0	1463	2	T18386 latrophilin-2 (spl)
32	2596.5	56.9	1399	2	T18370 latrophilin-2 (spl)
33	2596.5	56.9	1465	2	T18384 latrophilin-2 (spl)
34	2580	56.5	1412	2	T18380 latrophilin-2 (spl)
35	2580	56.5	1478	2	T18388 latrophilin-2 (spl)
36	2577	56.5	1420	2	T17158 CL2AB protein - ra
37	2554.5	56.0	1435	2	T46611 CL2AB protein - ra
38	2549.5	55.9	1463	2	T17159 CL2AC protein - ra
39	2527	55.4	1478	2	T17185 CL2BC protein - ra
40	2521	55.2	1452	2	T17157 CL2BA protein - ra
41	2518.5	55.2	1487	2	T14324 alpha-latrotoxin r
42	2498.5	54.8	1467	2	T17160 CL2BA protein - ra
43	2158	47.3	1466	2	T17139 CL1AA protein - ra
44	2158	47.3	1471	2	T17149 CL1BA protein - ra
45	2148.5	47.1	1467	2	T18411 latrophilin-1, bra

ALIGNMENTS

RESULT 1

T18389 latrophilin-3, splice variant abaf, brain-specific - bovine

C:Species: Bos primigenius taurus (cattle)

C>Date: 15-Oct-1999 #sequence_revision 15-Oct-1999 #text_change 18-Feb-2000

C:Accession: T18389

R:Matsumita, H.; Leljanova, V.G.; Uskaryov, Y.A.

FEBS Lett. 443, 348-352, 1999

A>Title: The latrophilin family: multiply spliced G protein-coupled receptors with di

A:Reference number: T18869; MUID:99148828; PMID:10025961

A:Accession: T18389

A>Status: preliminary; translated from GB/EMBL/DBU

A:Molecule type: mRNA

A:Residues: 1-1503 <MAT>

A:Cross-references: EMBL:AF11085; NID:94164052; PID:94164053; PIDN:AD05321.1

C:Superfamily: alpha-latrotoxin receptor, calcium-independent

C:Keywords: alternative splicing; G protein-coupled receptor

Query Match	97.7%	Score 4456;	DB 2;	Length 1503;
Best Local Similarity	92.8%	Pred. No. 1.1e-309;		
Matches	861;	Conservative	3;	Mismatches 8;
			Indels	56;
			Gaps	2;
QY	1	AEQTRNHLNAGDITYSVRAMQVGLDVLNLPFGKDSARSINK	-----	48
DB	576	AEQTRNHLNAGDITYSVRAMQVGLDVLNLPFGKDSARSINKLQKRESCRAY		635
QY	49	-AMVEYNNLLOPOLNLMARDLTSDDLRAATMLHFEESAFVLADMLKTDIYRENTD		107
DB	636	QAMVETVNNLLOPOLNLMARDLTSDDLRAATMLDIVEESAFVLADMLKTDIYRENTD		695
QY	108	NKLEVARLSTEGNLEDKPEPNMGHSTTQLSANTLKNONGRNGEIRVAFLVYNNLGPYL		167
DB	696	NKLEVARLSTEGNLEDKPEPNMGHSTTQLSANTLKNONGRNGEIRVAFLVYNNLGPYL		755
QY	168	STENASMKLGTFTALSTNHSVIVNSPYTAITAKESNSKVIYLAADPVVFYVTKHKOSEENFN		227
DB	756	STENASMKLGTFTAMSTNHSVIVNSPYTAITAKESNSKVIYLAADPVVFYVTKHKOSEENFN		815
QY	228	PCGSFWSKRTMTGYWSFOGCRLLTNTKTHHTGSCNHLNTPAVLMAHVEVKSADVDL		287
DB	816	PCGSFWSKRTMTGYWSFOGCRLLTNTKTHHTGSCNHLNTPAVLMAHVEVKSADVDL		875
QY	288	LIDVITWVGILSLVCLDICTFPCFPGLOSDDMTIHKNICISLFAVELFLIGINRTD		347
DB	876	LIDVITWVGILSLVCLDICTFPCFPGLOSDDMTIHKNICISLFAVELFLIGINRTD		935
QY	348	QPIACAVFAALHFFFLAFTMFLFEGVOLYIMLVEVESEHSRRKRYLVGSGPALIV		407
DB	936	QPIACAVFAALHFFFLAFTMFLFEGVOLYIMLVEVESEHSRRKRYLVGSGPALIV		995
QY	408	AVSAVDRSGYGVKVRDLDTYFIWSPFGPATLIMLVFLIALYKMFHFAIKP		467

Db 996 AVSAADVRSYGTGDKVCMRLDTYFTWSEFGPATLLIMLVIFLGIALYKMFHHTAILKP 1055
Qy 468 ESGCLDNKISWVIGATALLCLGLTWAFGLMYINESTVIMAYLFTFNSIQGFIFHC 527
Db 1056 ESGCLDNKISWVIGATALLCLGLTWAFGLMYINESTVIMAYLFTFNSIQGFIFHC 1115
Qy 528 VLOKKVREKYGKCLRTHCCSGKSTESSIGSGKTSGSRTPGRTGYSQSRIIRMMNDTVRK 587
Db 1116 VLOKKVREKYGKCLRTHCCSGKSTESSIGSGKTSGSRTPGRTGYSQSRIIRMMNDTVRK 1175
Qy 588 QSESSFTGDIINSASLNR----- 606
Db 1176 QSESSFTGDIINSASLNR----- 606
Qy 607 --EGLLNARDTSVMDTLPPLNGHNGNSYSTASGEYLSNCVOIIDRGYNHNETALEKKILK 664
Db 1236 AOGGLLNARDTSVMDTLPPLNGHNGNSYSTASGEYLSNCVOIIDRGYNHNETALEKKILK 1295
Qy 665 ELTSNVIPTSLNNHERSSSEONRLMKLVNNGSGREDDAIVLDATSFNHEESLGLLELI 724
Db 1296 ELTSNVIPTSLNNHERSSSEONRLMKLVNNGSGREDDAIVLDATSFNHEESLGLLELI 1355
Qy 725 HEESDAPLLPRPVYSTENHOPHHYTRRRIPQDHSESFPLLTNEHEDLOSPPRDSLYTS 784
Db 1356 HEESDAPLLPRPVYSTENHOPHHYTRRRIPQDHSESFPLLTNEHEDLOSPPRDSLYTS 1415
Qy 785 MPFLAGVAATESVTSTQTPRPPAKCGDAEDVYKSMPLNGSRNHVHOLHTYYQLGRSS 844
Db 1416 MPFLAGVPAEASVTSTQTPRPPAKCGDAEDVYKSMPLNGSRNHVHOLHTYYQLGRSS 1475
Qy 845 DGFIVPPNKDGTPESSSKGPAHLVTSL 872
Db 1476 DGFIVPPNKDGTPESSSKGPAHLVTSL 1503

RESULT 2

T18395
latrophilin-3, splice variant dbaf, brain-specific - bovine
C:Species: Bos primigenius taurus (cattle)
C>Date: 15-Oct-1999 #sequence_revision 15-Oct-1999 #text_change 18-Feb-2000
C:Accession: T18395
R:Matsumita, H.; Lellanova, V.G.; Ushkaryov, Y.A.
FEBS Lett. 443, 348-352, 1999
A>Title: The latrophilin family: multiply spliced G protein-coupled receptors with differ
A:Reference number: Z18869; MUID:99148828; PMID:10025961
A:Accession: T18395
A:Status: preliminary; translated from GB/EMBL/DBJ
A:Molecule type: mRNA
A:Residues: 1-1571 <MAT>
A:Cross-references: EMBL:AF111091; NID:94164064; PID:94164065; PIDN:AAD05327.1
C:Superfamily: alpha-latotoxin receptor, calcium-independent
C:Keywords: alternative splicing; G protein-coupled receptor

Query Match 97.7%; Score 4456; DB 2; Length 1571;
Best Local Similarity 92.8%; Pred. No. 1.2e-309;
Matches 861; Conservative 3; Mismatches 8; Indels 56; Gaps 2;
Qy 1 AEOIRHNLNAGDITTVSRAMDOLVGLLDVQRLNLTGPGKDSARSLNK----- 48
Db 644 AEOIRHNLNAGDITTVSRAMDOLVGLLDVQRLNLTGPGKDSARSLNKLOKKRSCRAY 703
Qy 49 -AMVETVNNLLOPQALNARDLTTSDQLRAATMLHTVESAFVLADNLKTDIVEND 107
Db 704 QAMVETVNNLLOPQALNARDLTTSDQLRAATMLHTVESAFVLADNLKTDIVEND 763
Qy 108 NIKLEVARLSTEGNEDLKPEPMKGSTIQLSANTLKONGRGEIRVAVLYNNIGPYL 167
Db 764 NIOLEVARLSTEGNEDLKPEPMKGSTIQLSANTLKONGRGEIRVAVLYNNIGPYL 823
Qy 168 STENASMKLSTEGNEDLKPEPMKGSTIQLSANTLKONGRGEIRVAVLYNNIGPYL 227
Db 824 STENASMKLSTEGNEDLKPEPMKGSTIQLSANTLKONGRGEIRVAVLYNNIGPYL 883

Qy 228 PNCSEFMSYKRTMTGYWSTOGCRLLTNTKHTTSCNHLTNFAVLMAHVEVKSADVHDL 287
Db 884 PNCSEFMSYKRTMTGYWSTOGCRLLTNTKHTTSCNHLTNFAVLMAHVEVKSADVHDL 943
Qy 288 LLDVITWVGILLSLVCLLCIFTFCEFRGIQSQRNTIHKNLCLSLVAELFLIGINRFD 347
Db 944 LLDVITWVGILLSLVCLLCIFTFCEFRGIQSQRNTIHKNLCLSLVAELFLIGINRFD 1003
Qy 348 QPIACAVFALLHFFFLAFTWMELEGVOLYIMLVFESHSRRRYFLVYGMPALLY 407
Db 1004 QPIACAVFALLHFFFLAFTWMELEGVOLYIMLVFESHSRRRYFLVYGMPALLY 1063
Qy 408 AVSAADVRSYGTGDKVCMRLDTYFTWSEFGPATLLIMLVIFLGIALYKMFHHTAILKP 467
Db 1064 AVSAADVRSYGTGDKVCMRLDTYFTWSEFGPATLLIMLVIFLGIALYKMFHHTAILKP 1123
Qy 468 ESGCLDNKISWVIGATALLCLGLTWAFGLMYINESTVIMAYLFTFNSIQGFIFHC 527
Db 1124 ESGCLDNKISWVIGATALLCLGLTWAFGLMYINESTVIMAYLFTFNSIQGFIFHC 1183
Qy 528 VLOKKVREKYGKCLRTHCCSGKSTESSIGSGKTSGSRTPGRTGYSQSRIIRMMNDTVRK 587
Db 1184 VLOKKVREKYGKCLRTHCCSGKSTESSIGSGKTSGSRTPGRTGYSQSRIIRMMNDTVRK 1243
Qy 588 QSESSFTGDIINSASLNR----- 606
Db 1244 QSESSFTGDIINSASLNR----- 606
Qy 607 --EGLLNARDTSVMDTLPPLNGHNGNSYSTASGEYLSNCVOIIDRGYNHNETALEKKILK 664
Db 1304 AOGGLLNARDTSVMDTLPPLNGHNGNSYSTASGEYLSNCVOIIDRGYNHNETALEKKILK 1363
Qy 665 ELTSNVIPTSLNNHERSSSEONRLMKLVNNGSGREDDAIVLDATSFNHEESLGLLELI 724
Db 1364 ELTSNVIPTSLNNHERSSSEONRLMKLVNNGSGREDDAIVLDATSFNHEESLGLLELI 1423
Qy 725 HEESDAPLLPRPVYSTENHOPHHYTRRRIPQDHSESFPLLTNEHEDLOSPPRDSLYTS 784
Db 1424 HEESDAPLLPRPVYSTENHOPHHYTRRRIPQDHSESFPLLTNEHEDLOSPPRDSLYTS 1483
Qy 785 MPFLAGVAATESVTSTQTPRPPAKCGDAEDVYKSMPLNGSRNHVHOLHTYYQLGRSS 844
Db 1484 MPFLAGVPAEASVTSTQTPRPPAKCGDAEDVYKSMPLNGSRNHVHOLHTYYQLGRSS 1543
Qy 845 DGFIVPPNKDGTPESSSKGPAHLVTSL 872
Db 1544 DGFIVPPNKDGTPESSSKGPAHLVTSL 1571

RESULT 3

T18392
latrophilin-3, splice variant abdf, brain-specific - bovine
C:Species: Bos primigenius taurus (cattle)
C>Date: 15-Oct-1999 #sequence_revision 15-Oct-1999 #text_change 18-Feb-2000
C:Accession: T18392
R:Matsumita, H.; Lellanova, V.G.; Ushkaryov, Y.A.
FEBS Lett. 443, 348-352, 1999
A>Title: The latrophilin family: multiply spliced G protein-coupled receptors with di
A:Reference number: Z18869; MUID:99148828; PMID:10025961
A:Accession: T18392
A:Status: preliminary; translated from GB/EMBL/DBJ
A:Molecule type: mRNA
A:Residues: 1-1512 <MAT>
A:Cross-references: EMBL:AF111088; NID:94164058; PID:94164059; PIDN:AAD05324.1
C:Superfamily: alpha-latotoxin receptor, calcium-independent
C:Keywords: alternative splicing; G protein-coupled receptor

Query Match 97.3%; Score 4441.5; DB 2; Length 1512;
Best Local Similarity 91.9%; Pred. No. 1.2e-308;
Matches 861; Conservative 3; Mismatches 8; Indels 65; Gaps 3;
Qy 1 AEOIRHNLNAGDITTVSRAMDOLVGLLDVQRLNLTGPGKDSARSLNK----- 48

Db 576 AEQTRHNLNAGDITTVSVRAMDQVLGLDVOLRLMTPGCKDSAAARSINKLQKRERSGRAY 635
 QY 49 -AMETVNNLLOPOLANMWDLTTSQDLRAATMLHTVEESAVFLADNLKTDIVREND 107
 Db 636 QAAVEVNNLLOPOLANMWDLTTSQDLRAATMLHTVEESAVFLADNLKTDIVREND 695
 QY 108 NIKLEVARLSTEGNLEDLKREPMKGGSTQLSANTLKONGRGEIRVAVFLVNNLGPYL 167
 Db 696 NIKLEVARLSTEGNLEDLKREPMKGGSTQLSANTLKONGRGEIRVAVFLVNNLGPYL 755
 QY 168 STENASMKLGTALSTNHSIVNSPVITAAINKEFSNKVYLADPVVFTYKHIOSEENFN 227
 Db 756 STENASMKLGTALSTNHSIVNSPVITAAINKEFSNKVYLADPVVFTYKHIOSEENFN 815
 QY 228 PNCSEFMSYSKRTMTGWSTOGCRLLTNTKTHTCSCNHLTNFAVLMAHVEVKHSDAVHDL 287
 Db 816 PNCSEFMSYSKRTMTGWSTOGCRLLTNTKTHTCSCNHLTNFAVLMAHVEVKHSDAVHDL 875
 QY 288 LLDVITWVGILSLVCLLCIFTECFEFGILOSDRNTIHKMLCISLVEAELLFLGINKRD 347
 Db 876 LLDVITWVGILSLVCLLCIFTECFEFGILOSDRNTIHKMLCISLVEAELLFLGINKRD 935
 QY 348 QPIACAVFAALLHFFFLAFTWMLFEGVOLYIMLVEVESEHSRRKRYFYLVGYGMPALIV 407
 Db 936 QPIACAVFAALLHFFFLAFTWMLFEGVOLYIMLVEVESEHSRRKRYFYLVGYGMPALIV 995
 QY 408 AVSAADYRSYGTDKYCMRLDITYFTWSPFGPATLLIMLVIFLGIALYKMFHHTAILKP 467
 Db 996 AVSAADYRSYGTDKYCMRLDITYFTWSPFGPATLLIMLVIFLGIALYKMFHHTAILKP 1055
 QY 468 ESCGLDN-----IKSWAIGAILCLLGLTMAFGLMYINESVYIMAYLFTINSIQ 518
 Db 1056 ESCGLDNINEDNRPFIKSVIGAILCLLGLTMAFGLMYINESVYIMAYLFTINSIQ 1115
 QY 519 GMFIFIFHCYLOKKVREYKCLRTHCSCGSTESSIGSKTSGSRTPGRYSTGQSRRIR 578
 Db 1116 GMFIFIFHCYLOKKVREYKCLRTHCSCGSTESSIGSKTSGSRTPGRYSTGQSRRIR 1175
 QY 579 RMNDVVRKOSSEFFITGDINSSASLNR----- 606
 Db 1176 RMNDVVRKOSSEFFITGDINSSASLNRGMANHLISNALLRPHGTNNPYNTLLGEPAYC 1235
 QY 607 -----EGLNNARDTSYMDTLPLNGNNGNSYIASGEYLSNCVOIIDRGYNHNE 655
 Db 1236 NNSVSMTYNAQEBGLNNARPTSYMDTLPLNGNNGNSYIASGEYLSNCVOIIDRGYNHNE 1295
 QY 656 TALEKKILKELTSNYIPSYLNNHERSEONRNLMKLVNMLGSGREDDAIVLDDATSPFNH 715
 Db 1296 TALEKKILKELTSNYIPSYLNNHERSEONRNLMKLVNMLGSGREDDAIVLDDATSPFNH 1355
 QY 716 EESLGLLELHESDAPLPRRYVSTENHOPNHTTRRIIPQDHSESPFLLTNEHTEDLOS 775
 Db 1356 EESLGLLELHESDAPLPRRYVSTENHOPNHTTRRIIPQDHSESPFLLTNEHTEDLOS 1415
 QY 776 PHNDSLYTSMPTLAGVAALIESVTTSTQTEPPRAKCGDAEDVYKSMNPNGSRNHVQLHT 835
 Db 1416 PHNDSLYTSMPTLAGVAALIESVTTSTQTEPPRAKCGDAEDVYKSMNPNGSRNHVQLHT 1475
 QY 836 YVOLGRSSDGFIVPNNKDGTPREGSSKGPANLVTSL 872
 Db 1476 YVOLGRSSDGFIVPNNKDGTPREGSSKGPANLVTSL 1512

RESULT 4

T18407
 latrophilin-3, splice variant bdbf, brain-specific - bovine
 C:Species: Bos primigenius taurus (cattle)
 C:Date: 15-Oct-1999 #sequence_revision 15-Oct-1999 #text_change 18-Feb-2000
 C:Accession: T18407
 R:Matsumita, H.; Ielianaova, V.G.; Ushkaryov, Y.A.
 FEBS Lett. 443, 348-352, 1999
 A:Title: The latrophilin family: multiply spliced G protein-coupled receptors with differ
 A:Reference number: Z18869; MUID:99148828; PMID:10025961

A:Accession: T18407
 A:Status: preliminary; translated from GB/EMBL/DBJ
 A:Molecule type: mRNA
 A:Residues: 1-1580 <Mat>
 A:Cross-references: EMBL:AF111094; NID:94164070; PID:94164071; PIDN:AAD05330.1
 C:Superfamily: alpha-latrotoxin receptor, calcium-independent
 C:Keywords: alternative splicing; G protein-coupled receptor
 Query Match 97.3%; Score 4441.5; DB 2; Length 1580;
 Best Local Similarity 91.9%; Pred. No. 1.3e-308;
 Matches 861; Conservative 3; Mismatches 8; Indels 65; Gaps 3;
 QY 1 AEQTRHNLNAGDITTVSVRAMDQVLGLDVOLRLMTPGCKDSAAARSINKLQKRERSGRAY 48
 Db 644 AEQTRHNLNAGDITTVSVRAMDQVLGLDVOLRLMTPGCKDSAAARSINKLQKRERSGRAY 703
 QY 49 -AMETVNNLLOPOLANMWDLTTSQDLRAATMLHTVEESAVFLADNLKTDIVREND 107
 Db 704 QAAVEVNNLLOPOLANMWDLTTSQDLRAATMLHTVEESAVFLADNLKTDIVREND 763
 QY 108 NIKLEVARLSTEGNLEDLKREPMKGGSTQLSANTLKONGRGEIRVAVFLVNNLGPYL 167
 Db 764 NIKLEVARLSTEGNLEDLKREPMKGGSTQLSANTLKONGRGEIRVAVFLVNNLGPYL 823
 QY 168 STENASMKLGTALSTNHSIVNSPVITAAINKEFSNKVYLADPVVFTYKHIOSEENFN 227
 Db 824 STENASMKLGTALSTNHSIVNSPVITAAINKEFSNKVYLADPVVFTYKHIOSEENFN 883
 QY 228 PNCSEFMSYSKRTMTGWSTOGCRLLTNTKTHTCSCNHLTNFAVLMAHVEVKHSDAVHDL 287
 Db 884 PNCSEFMSYSKRTMTGWSTOGCRLLTNTKTHTCSCNHLTNFAVLMAHVEVKHSDAVHDL 943
 QY 288 LLDVITWVGILSLVCLLCIFTECFEFGILOSDRNTIHKMLCISLVEAELLFLGINKRD 347
 Db 944 LLDVITWVGILSLVCLLCIFTECFEFGILOSDRNTIHKMLCISLVEAELLFLGINKRD 1003
 QY 348 QPIACAVFAALLHFFFLAFTWMLFEGVOLYIMLVEVESEHSRRKRYFYLVGYGMPALIV 407
 Db 1004 QPIACAVFAALLHFFFLAFTWMLFEGVOLYIMLVEVESEHSRRKRYFYLVGYGMPALIV 1063
 QY 408 AVSAADYRSYGTDKYCMRLDITYFTWSPFGPATLLIMLVIFLGIALYKMFHHTAILKP 467
 Db 1064 AVSAADYRSYGTDKYCMRLDITYFTWSPFGPATLLIMLVIFLGIALYKMFHHTAILKP 1123
 QY 468 ESCGLDN-----IKSWAIGAILCLLGLTMAFGLMYINESVYIMAYLFTINSIQ 518
 Db 1124 ESCGLDNINEDNRPFIKSVIGAILCLLGLTMAFGLMYINESVYIMAYLFTINSIQ 1183
 QY 519 GMFIFIFHCYLOKKVREYKCLRTHCSCGSTESSIGSKTSGSRTPGRYSTGQSRRIR 578
 Db 1184 GMFIFIFHCYLOKKVREYKCLRTHCSCGSTESSIGSKTSGSRTPGRYSTGQSRRIR 1243
 QY 579 RMNDVVRKOSSEFFITGDINSSASLNR----- 606
 Db 1244 RMNDVVRKOSSEFFITGDINSSASLNRGMANHLISNALLRPHGTNNPYNTLLGEPAYC 1303
 QY 607 -----EGLNNARDTSYMDTLPLNGNNGNSYIASGEYLSNCVOIIDRGYNHNE 655
 Db 1304 NNSVSMTYNAQEBGLNNARPTSYMDTLPLNGNNGNSYIASGEYLSNCVOIIDRGYNHNE 1363
 QY 656 TALEKKILKELTSNYIPSYLNNHERSEONRNLMKLVNMLGSGREDDAIVLDDATSPFNH 715
 Db 1364 TALEKKILKELTSNYIPSYLNNHERSEONRNLMKLVNMLGSGREDDAIVLDDATSPFNH 1423
 QY 716 EESLGLLELHESDAPLPRRYVSTENHOPNHTTRRIIPQDHSESPFLLTNEHTEDLOS 775
 Db 1424 EESLGLLELHESDAPLPRRYVSTENHOPNHTTRRIIPQDHSESPFLLTNEHTEDLOS 1483
 QY 776 PHNDSLYTSMPTLAGVAALIESVTTSTQTEPPRAKCGDAEDVYKSMNPNGSRNHVQLHT 835
 Db 1484 PHNDSLYTSMPTLAGVAALIESVTTSTQTEPPRAKCGDAEDVYKSMNPNGSRNHVQLHT 1543
 QY 836 YVOLGRSSDGFIVPNNKDGTPREGSSKGPANLVTSL 872

Db 1544 YVOLGRSSSDGFIVPPNKGDPPEGSSSGPAHLVTSL 1580

RESULT 5

T17186

CL3A protein - rat

C:Species: Rattus norvegicus (Norway rat)

C>Date: 15-Oct-1999 #sequence_revision 15-Oct-1999 #text_change 18-Feb-2000

C:Accession: T17186

R:Sugita, S.; Ichikhenko, K.; Khvotchev, M.; Sudhof, T.C.

submitted to the EMBL Data Library, July 1998

A:Description: CL family.

A:Reference number: Z18712

A:Accession: T17186

A:Molecule type: mRNA

A:Status: preliminary; translated from GB/EMBL/DBJ

A:Residues: 1-1459 <SUG>

A:Cross-references: EMBL:AF081154; NID:g3695134; PID:g3695135; PIDN:MAC62660.1

C:Superfamily: alpha-latrotoxin receptor, calcium-independent

Query Match

Best Local Similarity 95.5%; Score 4401.5; DB 2; Length 1459;

Matches 845; Conservative 10; Mismatches 17; Indels 13; Gaps 1;

Query 1 AEOTRNHLNMGDIYVRAMQDLVGLDVLQRLNLTGGKDSAAKSLNK----- 48

Db 575 AEOTRNHLNMGDIYVRAMQDLVGLDVLQRLNLTGGKDSAAKSLNKLOKRESCRAY 634

Db 49 -AMEYEVNNTLQPOLANARDLTSDOLRAATMLLHYEESAFVLADNLKTDIVRENTD 107

Db 635 QAMEYEVNNTLQPOLANARDLTSDOLRAATMLLHYEESAFVLADNLKTDIVRENTD 694

Db 108 NIKLEVARLSTEGNLEDLKPEPNMGHSTIQLSANTLKONGRGEIRAFVLYNNLGPYL 167

Db 695 NIOLEVARLSTEGNLEDLKPEPNMGHSTIQLSANTLKONGRGEIRAFVLYNNLGPYL 754

Db 168 STENASKKLGTALSTNHSIVNSPVITTAANKESNKVYLADVPVTFVKHIKSEENFN 227

Db 755 STENASKKLGTALSTNHSIVNSPVITTAANKESNKVYLADVPVTFVKHIKSEENFN 814

Db 228 PNCFSWYSKRTMTGYSTOGCRLLTNTKHTTSCNHLTFNFAVLMHVEKHSDAVHDL 287

Db 815 PNCFSWYSKRTMTGYSTOGCRLLTNTKHTTSCNHLTFNFAVLMHVEKHSDAVHDL 874

Db 288 LLDVITWVGILLSLVCLLICTFECFFRGLOSDRNTIHKNCISLFAVELLFLGINRTD 347

Db 875 LLDVITWVGILLSLVCLLICTFECFFRGLOSDRNTIHKNCISLFAVELLFLGINRTD 934

Db 348 QPIACAVFAALLHFFLAFTWMLFEGVOLYIMLVEVESESHSRKRYFYLVGYMPALIV 407

Db 935 QPIACAVFAALLHFFLAFTWMLFEGVOLYIMLVEVESESHSRKRYFYLVGYMPALIV 994

Db 408 AVSAADVRSYGTGDKVCMRLDTYFIMSFIGPATLIMLANVIFGIALYKMFHTTALIKP 467

Db 995 AVSAADVRSYGTGDKVCMRLDTYFIMSFIGPATLIMLANVIFGIALYKMFHTTALIKP 1054

Db 468 ESGCLDINKSVIGAILLCLGLTMAFGMLYINESTVIMAYLFTFNSLOGMFIPTFHC 527

Db 1055 ESGCLDINKSVIGAILLCLGLTMAFGMLYINESTVIMAYLFTFNSLOGMFIPTFHC 1114

Db 528 VLOKVRKREYKCLRTKCCSGKSTRESSIGSGKTSRTPGRYSGTSGOSRIIRMMNDTVRK 587

Db 1115 VLOKVRKREYKCLRTKCCSGKSTRESSIGSGKTSRTPGRYSGTSGOSRIIRMMNDTVRK 1174

Db 588 QSESSFTTGDINSASLNREGLNNARDYSMDTLPPLNGHNSYSLASGEYLSNCVOII 647

Db 1175 QSESSFTTGDINSASLNREGLNNARDYSMDTLPPLNGHNSYSLASGEYLSNCVOII 1234

Db 648 DRGNHNEFTALEKKILKELTSNYIPSYLNNHERSSDONRLMANKLVNNGSGRDDDAIVL 707

Db 1235 DRGNHNEFTALEKKILKELTSNYIPSYLNNHERSSDONRLMANKLVNNGSGRDDDAIVL 1294

Qy 708 DDATSFNHEESLGLLHEESDAPLPPRYVSTENHOPHHYTRRRIRQDHSSEFPPLTN 767

Db 1295 DDATSFNHEESLGLLHEESDAPLPPRYVSTENHOPHHYTRRRIRQDHSSEFPPLTN 1354

Qy 768 EHTEDLOSPPHDSLYTSPNLAGVAATESYTTSTQTERPPKACDADYVYKSPNIGSR 827

Db 1355 EHTEDLOSPPHDSLYTSPNLAGVAATESYTTSTQTERPPKACDADYVYKSPNIGSR 1414

Qy 828 NHHVHLTHYYOLGRGSSDGFIVPPNKGDPPEGSSSGPAHLVTSL 872

Db 1415 NHHVHLTHYYOLGRGSSDGFIVPPNKGDPPEGSSSGPAHLVTSL 1459

RESULT 6

T17198

CL3A protein - rat

C:Species: Rattus norvegicus (Norway rat)

C>Date: 15-Oct-1999 #sequence_revision 15-Oct-1999 #text_change 04-Mar-2000

C:Accession: T17198

R:Sugita, S.; Ichikhenko, K.; Khvotchev, M.; Sudhof, T.C.

submitted to the EMBL Data Library, July 1998

A:Description: CL family.

A:Reference number: Z18712

A:Accession: T17198

A:Molecule type: mRNA

A:Status: preliminary; translated from GB/EMBL/DBJ

A:Residues: 1-1527 <SUG>

A:Cross-references: EMBL:AF081157; NID:g3695140; PID:g3695141; PIDN:MAC62663.1

C:Superfamily: alpha-latrotoxin receptor, calcium-independent

Query Match

Best Local Similarity 95.5%; Score 4401.5; DB 2; Length 1527;

Matches 845; Conservative 10; Mismatches 17; Indels 13; Gaps 1;

Query 1 AEOTRNHLNMGDIYVRAMQDLVGLDVLQRLNLTGGKDSAAKSLNK----- 48

Db 643 AEOTRNHLNMGDIYVRAMQDLVGLDVLQRLNLTGGKDSAAKSLNKLOKRESCRAY 702

Db 49 -AMEYEVNNTLQPOLANARDLTSDOLRAATMLLHYEESAFVLADNLKTDIVRENTD 107

Db 703 QAMEYEVNNTLQPOLANARDLTSDOLRAATMLLHYEESAFVLADNLKTDIVRENTD 762

Db 108 NIKLEVARLSTEGNLEDLKPEPNMGHSTIQLSANTLKONGRGEIRAFVLYNNLGPYL 167

Db 763 NIOLEVARLSTEGNLEDLKPEPNMGHSTIQLSANTLKONGRGEIRAFVLYNNLGPYL 822

Db 168 STENASKKLGTALSTNHSIVNSPVITTAANKESNKVYLADVPVTFVKHIKSEENFN 227

Db 823 STENASKKLGTALSTNHSIVNSPVITTAANKESNKVYLADVPVTFVKHIKSEENFN 882

Db 228 PNCFSWYSKRTMTGYSTOGCRLLTNTKHTTSCNHLTFNFAVLMHVEKHSDAVHDL 287

Db 883 PNCFSWYSKRTMTGYSTOGCRLLTNTKHTTSCNHLTFNFAVLMHVEKHSDAVHDL 942

Db 288 LLDVITWVGILLSLVCLLICTFECFFRGLOSDRNTIHKNCISLFAVELLFLGINRTD 347

Db 943 LLDVITWVGILLSLVCLLICTFECFFRGLOSDRNTIHKNCISLFAVELLFLGINRTD 1002

Db 348 QPIACAVFAALLHFFLAFTWMLFEGVOLYIMLVEVESESHSRKRYFYLVGYMPALIV 407

Db 1003 QPIACAVFAALLHFFLAFTWMLFEGVOLYIMLVEVESESHSRKRYFYLVGYMPALIV 1062

Db 408 AVSAADVRSYGTGDKVCMRLDTYFIMSFIGPATLIMLANVIFGIALYKMFHTTALIKP 467

Db 1063 AVSAADVRSYGTGDKVCMRLDTYFIMSFIGPATLIMLANVIFGIALYKMFHTTALIKP 1122

Db 468 ESGCLDINKSVIGAILLCLGLTMAFGMLYINESTVIMAYLFTFNSLOGMFIPTFHC 527

Db 1123 ESGCLDINKSVIGAILLCLGLTMAFGMLYINESTVIMAYLFTFNSLOGMFIPTFHC 1182

Db 528 VLOKVRKREYKCLRTKCCSGKSTRESSIGSGKTSRTPGRYSGTSGOSRIIRMMNDTVRK 587

Db 1183 VLOKVRKREYKCLRTKCCSGKSTRESSIGSGKTSRTPGRYSGTSGOSRIIRMMNDTVRK 1242

QY 588 QSESEFTGDIINSASLNREGILNNARDTSVMDTLPUNGNGNSYSIASEYLNCVQII 647
|||||
Db 1243 QSSSSFTIGDINSASLNREGILNNARDTSVMDTLPUNGNGNSYSIASEYLNCVQII 1302
QY 648 DRGYNHETALEKKILKELTSNYIPSYLNHHERSSQONRMKLVNMLSGREDAIVL 707
|||||
Db 1303 DRGYNHETALEKKILKELTSNYIPSYLNHHERSSQONRMKLVNMLSGREDAIVL 1362
QY 708 DDAATSTNHEESLGLLEIHEESDAPLLPRVYSTENHOPIHHYTRRRIPDHSSEFPPLLN 767
|||||
Db 1363 DDAATSTNHEESLGLLEIHEESDAPLLPRVYSTENHOPIHHYTRRRIPDHSSEFPPLLN 1422
QY 768 EHEEDQSPHRSIYSMTPLAGVAATFESTYSTOTEPRAKGDADVYKSGMPNLGSR 827
|||||
Db 1423 EHEEDQSPHRSIYSMTPLAGVAATFESTYSTOTEPRAKGDADVYKSGMPNLGSR 1482
QY 828 NHVHQLHTYVQLGRGSSDGFIVPNKDGTPREGSSKGAHALVTSL 872
|||||
Db 1483 NHVHQLHTYVQLGRGSSDGFIVPNKDGTPREGSSKGAHALVTSL 1527
RESULT 7
T14327
alpha-latrotoxin receptor 3, calcium-independent - rat
N:Alternate names: G-protein coupled receptor
C:Species: Rattus norvegicus (Norway rat)
C:Date: 20-Sep-1999 #sequence_revision 20-Sep-1999 #ext_change 18-Feb-2000
C:Accession: T14327
R:Ichchenko, K.A.; Biltner, M.A.; Krasnoperov, V.; Little, A.R.; Chepuray, O.; Holz, R.
J. Biol. Chem. 274, 5491-5498, 1999
A:Title: A novel ubiquitously expressed alpha-latrotoxin receptor is a member of the C1H
A:Reference number: Z17983; MIMD:99150330; PMID:10026162
A:Accession: T14327
A:Status: preliminary; translated from GB/EMBL/DBJ
A:Molecule type: mRNA
A:Residues: 1-1550 <ICH>
A:Cross-references: EMBL:AF063103; NID:93882980; PID:93882981; PIDN:AAC77816.1
C:Genetics:
A:Gene: C1RL-3
C:Superfamily: alpha-latrotoxin receptor, calcium-independent
Query Match 95.8%; Score 4370; DB 2; Length 1550;
Best Local Similarity 93.1%; Pred. No. 1.7e-303;
Matches 845; Conservative 10; Mismatches 17; Indels 36; Gaps 3;
QY 1 AEOGRNHLNAGDITTSVVRAMQDLVGLLDVQLRMLTPGKGKSAARSINK----- 48
|||||
Db 643 AEOGRNHLNAGDITTSVVRAMQDLVGLLDVQLRMLTPGKGKSAARSINKLQKRRCRAVY 702
QY 49 -AMVETVNNLLOQALNAMDLTTSQDLRAATMLLHTVESAFVLADNLKTIVREND 107
|||||
Db 703 QAMVETVNNLLOQALNAMDLTTSQDLRAATMLLHTVESAFVLADNLKTIVREND 762
QY 108 NIKLEVARLSTEGNLDLKFPEMNGHGSTTQLSANTLKQNGRGEIRVAFVLNNIGPYL 167
|||||
Db 763 NIKLEVARLSTEGNLDLKFPEMNGHGSTTQLSANTLKQNGRGEIRVAFVLNNIGPYL 822
QY 168 STENASMKLQTEALSTNHSIVNSPVITAAINKEFSNKVYLDPPVETVYKHIOSEENFN 227
|||||
Db 823 STENASMKLQTEALSTNHSIVNSPVITAAINKEFSNKVYLDPPVETVYKHIOSEENFN 882
QY 228 PNCSEFSYSKRMTGYWSVQGCRLTLTKTHHTCSGNHLTNFVLAHVEVKSADAVHL 287
|||||
Db 883 PNCSEFSYSKRMTGYWSVQGCRLTLTKTHHTCSGNHLTNFVLAHVEVKSADAVHL 942
QY 288 LLDVITWVGLLSTVCLLCIFTCFCEFGSDRNTIHKMLCSTLVAELFLIGINRTD 347
|||||
Db 943 LLDVITWVGLLSTVCLLCIFTCFCEFGSDRNTIHKMLCSTLVAELFLIGINRTD 1002
QY 348 QPIACAVFALLHFFFLAAFTMNLGEGVOLYIMLVEFESEHSRRRYFLVGYGMPALIV 407
|||||
Db 1003 QPIACAVFALLHFFFLAAFTMNLGEGVOLYIMLVEFESEHSRRRYFLVGYGMPALIV 1062

QY 408 AVSAADYRSYGTDXKCMRLDPTFTMSFTGPATLIIMLVIFLGTALYKMFHHTALPK 467
|||||
Db 1063 AVSAADYRSYGTDXKCMRLDPTFTMSFTGPATLIIMLVIFLGTALYKMFHHTALPK 1122
QY 468 ESQCLDN-----IKSVVIGAILCLLGLTMAFGMLYINESVYMAVLTFTNSIQ 518
|||||
Db 1123 ESQCLDNINEDNRPIKSVVIGAILCLLGLTMAFGMLYINESVYMAVLTFTNSIQ 1182
QY 519 GMFIFIFHCYLOKVRKEYGKCLRTGCCSGKSTRESSIGSKTSGSRTPGRYSTGQSRR 578
|||||
Db 1183 GMFIFIFHCYLOKVRKEYGKCLRTGCCSGKSTRESSIGSKTSGSRTPGRYSTGQSRR 1242
QY 579 RMMNDVVRKQSESSFTIGDINSASLNRGSLDPCQAVTYLGLLNNADTYSVMDTLP 624
|||||
Db 1243 RMMNDVVRKQSESSFTIGDINSASLNRGSLDPCQAVTYLGLLNNADTYSVMDTLP 1302
QY 625 NGNHGNSYSIASEYLSNCVQIIDRGYNHETALEKKILKELTSNYIPSYLNHHERSSQ 684
|||||
Db 1303 NGNHGNSYSIASEYLSNCVQIIDRGYNHETALEKKILKELTSNYIPSYLNHHERSSQ 1362
QY 685 NRMLMKNLVNMLSGREDAIVLDDATSFNHEESLGLLEIHEESDAPLLPRVYSTENHO 744
|||||
Db 1363 NRMLMKNLVNMLSGREDAIVLDDATSFNHEESLGLLEIHEESDAPLLPRVYSTENHO 1422
QY 745 PHHYTRRRIPQDHSSEFPPLLTNEHEDQSPHRSIYSMTPLAGVAATFESTYSTOTE 804
|||||
Db 1423 PHHYTRRRIPQDHSSEFPPLLTNEHEDQSPHRSIYSMTPLAGVAATFESTYSTOTE 1482
QY 805 PPAKSGDADVYKSKPNLGSRRNHYQLHTYVQLGRGSSDGFIVPNKDGTPREGSSK 864
|||||
Db 1483 PPAKSGDADVYKSKPNLGSRRNHYQLHTYVQLGRGSSDGFIVPNKDGTPREGSSK 1542
QY 865 PAHALVTSL 872
|||||
Db 1543 PAHALVTSL 1550
RESULT 8
T17188
CL3AC protein - rat
C:Species: Rattus norvegicus (Norway rat)
C:Date: 15-Oct-1999 #sequence_revision 15-Oct-1999 #ext_change 04-Mar-2000
C:Accession: T17188
R:Sugita, S.; Ichchenko, K.; Khvotchev, M.; Sudhof, T.C.
Submitted to the EMBL Data Library, July 1998
A:Description: CL family.
A:Reference number: Z18712
A:Accession: T17188
A:Status: preliminary; translated from GB/EMBL/DBJ
A:Molecule type: mRNA
A:Residues: 1-1273 <SUG>
A:Cross-references: EMBL:AF081156; NID:93695138; PID:93695139; PIDN:AAC62662.1
C:Superfamily: alpha-latrotoxin receptor, calcium-independent
Query Match 68.5%; Score 3123.5; DB 2; Length 1273;
Best Local Similarity 93.3%; Pred. No. 1.4e-214;
Matches 609; Conservative 8; Mismatches 15; Indels 21; Gaps 3;
QY 1 AEOGRNHLNAGDITTSVVRAMQDLVGLLDVQLRMLTPGKGKSAARSINK----- 48
|||||
Db 575 AEOGRNHLNAGDITTSVVRAMQDLVGLLDVQLRMLTPGKGKSAARSINKLQKRRCRAVY 634
QY 49 -AMVETVNNLLOQALNAMDLTTSQDLRAATMLLHTVESAFVLADNLKTIVREND 107
|||||
Db 635 QAMVETVNNLLOQALNAMDLTTSQDLRAATMLLHTVESAFVLADNLKTIVREND 694
QY 108 NIKLEVARLSTEGNLDLKFPEMNGHGSTTQLSANTLKQNGRGEIRVAFVLNNIGPYL 167
|||||
Db 695 NIKLEVARLSTEGNLDLKFPEMNGHGSTTQLSANTLKQNGRGEIRVAFVLNNIGPYL 754
QY 168 STENASMKLQTEALSTNHSIVNSPVITAAINKEFSNKVYLDPPVETVYKHIOSEENFN 227
|||||

Db 755 STENASKLIGTEAMSTHSHVIVNSPVITAAINKEFSNKVYLADVPVTFVHKIKOSENFN 814
QY 228 PNCSEFMSYKRTMTGYSTGCGRLTTNTKTHHTSCNHLTNFAVLMHVEKHSDAVHDL 287
Db 815 PNCSEFMSYKRTMTGYSTGCGRLTTNTKTHHTSCNHLTNFAVLMHVEKHSDAVHDL 874
QY 288 LLDVITWVGILLSLVCLLICITFCFPRGLOSDBNTIHKNLCSLFAVELLFLGINTD 347
Db 875 LLDVITWVGILLSLVCLLICITFCFPRGLOSDBNTIHKNLCSLFAVELLFLGINTD 934
QY 348 OPTACAVFAALLHFEFLAFTWMLFLEGVOLYIMLVEVESESHSRKRYLVGYGMPALIV 407
Db 935 OPTACAVFAALLHFEFLAFTWMLFLEGVOLYIMLVEVESESHSRKRYLVGYGMPALIV 994
QY 408 AVSAADVRSYGTGDKVCMRLDTYFIMSFIPATLIMLVNFIPLALYKMFHTALPK 467
Db 995 AVSAADVRSYGTGDKVCMRLDTYFIMSFIPATLIMLVNFIPLALYKMFHTALPK 1054
QY 468 ESGCLDIKSWYGAIALCLLGLTMAFGMLYINESTVIMAYLFTINSLOGMFIETPHC 527
Db 1055 ESGCLDIKSWYGAIALCLLGLTMAFGMLYINESTVIMAYLFTINSLOGMFIETPHC 1114
QY 528 VLOKKVREKYGKCLRTCCSGKSTESSIGSGKTSRPGRYSTGOSRIRRMNDIVRK 587
Db 1115 VLOKKVREKYGKCLRTCCSGKSTESSIGSGKTSRPGRYSTGOSRIRRMNDIVRK 1174
QY 588 QSESSFITGDINSASINREGLNNARDTSYMDTLPNGNHG--NSYSIASGE 638
Db 1175 QSESSFITGDINSASINRGTMANHLMNSMLLR-----HGTNPNYNTLLGE 1221

RESULT 9
T17200

CL3BC protein - rat
C:Species: Rattus norvegicus (Norway rat)
C:Date: 15-Oct-1999 #sequence_revision 15-Oct-1999 #text_change 18-Feb-2000
C:Accession: T17200
R:Sugita, S.; Ichitchenko, K.; Khvotchev, M.; Sudhof, T.C.
submitted to the EMBL Data Library, July 1998
A:Description: CL family.
A:Reference number: 218712
A:Accession: T17200
A:Status: Preliminary; translated from GB/EMBL/DBJ
A:Molecule type: mRNA
A:Residues: 1-1341 <SUG>
A:Cross-references: EMBL:AF081159; NID:G3695144; PID:G3695145; PIDN:AAC62655.1
C:Superfamily: alpha-latrotoxin receptor, calcium-independent

Query Match 68.5%; Score 3123.5; DB 2; Length 1341;
Best Local Similarity 93.3%; Pred. No. 1.6e-214;
Matches 609; Conservative 8; Mismatches 15; Indels 21; Gaps 3;

QY 1 AEOTRNHLNMGDITYSVRADQVLGLDYLRLNLTGPGKDSAAKSLK----- 48
Db 643 AEOTRNHLNMGDITYSVRADQVLGLDYLRLNLTGPGKDSAAKSLKLOKRESCRAV 702
QY 49 -AMETVNNLLQPOLANMRDLTTSQDLRAATMLLHTVESAFVLAADNLKTDIRRENTD 107
Db 703 QAMVETVNNLLQPOLANMRDLTTSQDLRAATMLLHTVESAFVLAADNLKTDIRRENTD 762
QY 108 NIKLEVARLSTEGNLEDLKPEPNKGHSQTOLSAANTLKONGRNGEIVAFVLYNNLGPYL 167
Db 763 NIKLEVARLSTEGNLEDLKPEPNKGHSQTOLSAANTLKONGRNGEIVAFVLYNNLGPYL 822
QY 168 STENASKLIGTEAMSTHSHVIVNSPVITAAINKEFSNKVYLADVPVTFVHKIKOSENFN 227
Db 823 STENASKLIGTEAMSTHSHVIVNSPVITAAINKEFSNKVYLADVPVTFVHKIKOSENFN 882
QY 228 PNCSEFMSYKRTMTGYSTGCGRLTTNTKTHHTSCNHLTNFAVLMHVEKHSDAVHDL 287
Db 883 PNCSEFMSYKRTMTGYSTGCGRLTTNTKTHHTSCNHLTNFAVLMHVEKHSDAVHDL 942
QY 288 LLDVITWVGILLSLVCLLICITFCFPRGLOSDBNTIHKNLCSLFAVELLFLGINTD 347

Db 943 LLDVITWVGILLSLVCLLICITFCFPRGLOSDBNTIHKNLCSLFAVELLFLGINTD 1002
QY 348 OPTACAVFAALLHFEFLAFTWMLFLEGVOLYIMLVEVESESHSRKRYLVGYGMPALIV 407
Db 1003 OPTACAVFAALLHFEFLAFTWMLFLEGVOLYIMLVEVESESHSRKRYLVGYGMPALIV 1062
QY 408 AVSAADVRSYGTGDKVCMRLDTYFIMSFIPATLIMLVNFIPLALYKMFHTALPK 467
Db 1063 AVSAADVRSYGTGDKVCMRLDTYFIMSFIPATLIMLVNFIPLALYKMFHTALPK 1122
QY 468 ESGCLDIKSWYGAIALCLLGLTMAFGMLYINESTVIMAYLFTINSLOGMFIETPHC 527
Db 1123 ESGCLDIKSWYGAIALCLLGLTMAFGMLYINESTVIMAYLFTINSLOGMFIETPHC 1182
QY 528 VLOKKVREKYGKCLRTCCSGKSTESSIGSGKTSRPGRYSTGOSRIRRMNDIVRK 587
Db 1183 VLOKKVREKYGKCLRTCCSGKSTESSIGSGKTSRPGRYSTGOSRIRRMNDIVRK 1242
QY 588 QSESSFITGDINSASINREGLNNARDTSYMDTLPNGNHG--NSYSIASGE 638
Db 1243 QSESSFITGDINSASINRGTMANHLMNSMLLR-----HGTNPNYNTLLGE 1289

RESULT 10
T17187

CL3AB protein - rat
C:Species: Rattus norvegicus (Norway rat)
C:Date: 15-Oct-1999 #sequence_revision 15-Oct-1999 #text_change 04-Mar-2000
C:Accession: T17187
R:Sugita, S.; Ichitchenko, K.; Khvotchev, M.; Sudhof, T.C.
submitted to the EMBL Data Library, July 1998
A:Description: CL family.
A:Reference number: 218712
A:Accession: T17187
A:Status: Preliminary; translated from GB/EMBL/DBJ
A:Molecule type: mRNA
A:Residues: 1-1230 <SUG>
A:Cross-references: EMBL:AF081155; NID:G3695136; PID:G3695137; PIDN:AAC62661.1
C:Superfamily: alpha-latrotoxin receptor, calcium-independent

Query Match 68.4%; Score 3123; DB 2; Length 1230;
Best Local Similarity 91.9%; Pred. No. 1.5e-214;
Matches 614; Conservative 8; Mismatches 20; Indels 26; Gaps 4;

QY 1 AEOTRNHLNMGDITYSVRADQVLGLDYLRLNLTGPGKDSAAKSLK----- 48
Db 575 AEOTRNHLNMGDITYSVRADQVLGLDYLRLNLTGPGKDSAAKSLKLOKRESCRAV 634
QY 49 -AMETVNNLLQPOLANMRDLTTSQDLRAATMLLHTVESAFVLAADNLKTDIRRENTD 107
Db 635 QAMVETVNNLLQPOLANMRDLTTSQDLRAATMLLHTVESAFVLAADNLKTDIRRENTD 694
QY 108 NIKLEVARLSTEGNLEDLKPEPNKGHSQTOLSAANTLKONGRNGEIVAFVLYNNLGPYL 167
Db 695 NIKLEVARLSTEGNLEDLKPEPNKGHSQTOLSAANTLKONGRNGEIVAFVLYNNLGPYL 754
QY 168 STENASKLIGTEAMSTHSHVIVNSPVITAAINKEFSNKVYLADVPVTFVHKIKOSENFN 227
Db 755 STENASKLIGTEAMSTHSHVIVNSPVITAAINKEFSNKVYLADVPVTFVHKIKOSENFN 814
QY 228 PNCSEFMSYKRTMTGYSTGCGRLTTNTKTHHTSCNHLTNFAVLMHVEKHSDAVHDL 287
Db 815 PNCSEFMSYKRTMTGYSTGCGRLTTNTKTHHTSCNHLTNFAVLMHVEKHSDAVHDL 874
QY 288 LLDVITWVGILLSLVCLLICITFCFPRGLOSDBNTIHKNLCSLFAVELLFLGINTD 347
Db 875 LLDVITWVGILLSLVCLLICITFCFPRGLOSDBNTIHKNLCSLFAVELLFLGINTD 934
QY 348 OPTACAVFAALLHFEFLAFTWMLFLEGVOLYIMLVEVESESHSRKRYLVGYGMPALIV 407
Db 935 OPTACAVFAALLHFEFLAFTWMLFLEGVOLYIMLVEVESESHSRKRYLVGYGMPALIV 994

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QY 408 AVSAANDYRSYGTDKVCMRLDPTFWSFICPATLIMLVIFGLALYKMFHHTAILKP 467
    |||||||
DB 995 AVSAANDYRSYGTDKVCMRLDPTFWSFICPATLIMLVIFGLALYKMFHHTAILKP 1054
QY 468 ESGCLDNKSWYIGAITALLCLGLTWAFLMAYINVESTVIMAYLFTFNSLQGMFIFPHC 527
    |||||||
DB 1055 ESGCLDNKSWYIGAITALLCLGLTWAFLMAYINVESTVIMAYLFTFNSLQGMFIFPHC 1114
QY 528 VLQKVRKRYGKCLRTHCSSGKSTESSIGSGRTSGRSTGQSOSIRRMNDTVRK 587
    |||||||
DB 1115 VLQKVRKRYGKCLRTHCSSGKSTESSIGSGRTSGRSTGQSOSIRRMNDTVRK 1174
QY 588 OSESSFTTGDINSSASLNEGLLNARDTSVMDTLPNGNHGNSYSIASGEYLSNCVOIT 647
    |||||||
DB 1175 OSESSFTTGDINSSASLNEGLLNARDTSVMDTLPNGNHGNSYSIASGEYLSNCVOIT 1221
QY 648 DRGYNHNE 655
    ||:|
DB 1222 CHGYSTTE 1229

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RESULT 11

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T17199
CL3BB protein - rat
C:Species: Rattus norvegicus (Norway rat)
C>Date: 15-Oct-1999 #sequence_revision 15-Oct-1999 #text_change 04-Mar-2000
C:Accession: T17199
R:Subsita, S.; Ichthenko, K.; Khvotchev, M.; Sudhof, T. C.
Submitted to the EMBL Data Library, July 1998
A:Description: CL family.
A:Reference number: 218712
A:Accession: T17199
A:Status: preliminary; translated from GB/EMBL/DBJ
A:Molecule type: mRNA
A:Residues: 1-1298 <SUG>
A:Cross-references: EMBL:AF081158; NID:g3695142; PID:g3695143; PIDN:AAC62664.1
C:Superfamily: alpha-latrotoxin receptor, calcium-independent

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Query Match 68.4%; Score 3123; DB 2; Length 1298;
Best Local Similarity 91.9%; Pred. No. 1.6e-214;
Matches 614; Conservative 8; Mismatches 20; Indels 26; Gaps 4;

QY 1 AEGTRNHLNAGDITTSVRAMDQVGLLDVQLRNLTPGKDSARSLSNK----- 48
DB 643 AEGTRNHLNAGDITTSVRAMDQVGLLDVQLRNLTPGKDSARSLSNKQKRESCRAY 702
QY 49 -AMETVNNLLOPOLANARDLTTSQDLRAATMLHTVEESAFVLADNLKTDIVREND 107
DB 703 QAMETVNNLLOPOLANARDLTTSQDLRAATMLHTVEESAFVLADNLKTDIVREND 762
QY 108 NIKLEVARLSTEGNLEDLKFPEPMGHSITOLSANTLKONGRNGEIRVAFVLYNNIGPYL 167
DB 763 NIKLEVARLSTEGNLEDLKFPEPMGHSITOLSANTLKONGRNGEIRVAFVLYNNIGPYL 822
QY 168 STENASMKLGTEALSTNHSVIVNSPVITAAINKEFSNKUYLADPVVETVKHIKQSEEN 227
DB 823 STENASMKLGTEALSTNHSVIVNSPVITAAINKEFSNKUYLADPVVETVKHIKQSEEN 882
QY 228 PNCSEFSYSKRMTGYSWGCGRLTNTKTHHTSCNHLTNFAVLAHVEVKHSDAVHDL 287
DB 883 PNCSEFSYSKRMTGYSWGCGRLTNTKTHHTSCNHLTNFAVLAHVEVKHSDAVHDL 942
QY 288 LLDVITWVIGILSLVCLLCITFCFGRLOSDRNTIHNKLCISLVAELFLIGINRND 347
DB 943 LLDVITWVIGILSLVCLLCITFCFGRLOSDRNTIHNKLCISLVAELFLIGINRND 1002
QY 348 OPIACAVFALLHFFELAAFTWMLFEGVOLYIMLVEFESEHSRRKXYFLVGYGMPALIV 407
DB 1003 OPIACAVFALLHFFELAAFTWMLFEGVOLYIMLVEFESEHSRRKXYFLVGYGMPALIV 1062
QY 408 AVSAANDYRSYGTDKVCMRLDPTFWSFICPATLIMLVIFGLALYKMFHHTAILKP 467
DB 1063 AVSAANDYRSYGTDKVCMRLDPTFWSFICPATLIMLVIFGLALYKMFHHTAILKP 1122

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QY 468 ESGCLDNKSWYIGAITALLCLGLTWAFLMAYINVESTVIMAYLFTFNSLQGMFIFPHC 527
    |||||||
DB 1123 ESGCLDNKSWYIGAITALLCLGLTWAFLMAYINVESTVIMAYLFTFNSLQGMFIFPHC 1182
QY 528 VLQKVRKRYGKCLRTHCSSGKSTESSIGSGRTSGRSTGQSOSIRRMNDTVRK 587
    |||||||
DB 1183 VLQKVRKRYGKCLRTHCSSGKSTESSIGSGRTSGRSTGQSOSIRRMNDTVRK 1242
QY 588 OSESSFTTGDINSSASLNEGLLNARDTSVMDTLPNGNHGNSYSIASGEYLSNCVOIT 647
    |||||||
DB 1243 OSESSFTTGDINSSASLNEGLLNARDTSVMDTLPNGNHGNSYSIASGEYLSNCVOIT 1289
QY 648 DRGYNHNE 655
    ||:|
DB 1290 CHGYSTTE 1297

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RESULT 12

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T18391
latrophilin-3, splice variant abah, brain-specific - bovine
C:Species: Bos primigenius taurus (cattle)
C>Date: 15-Oct-1999 #sequence_revision 15-Oct-1999 #text_change 18-Feb-2000
C:Accession: T18391
R:Matsushita, H.; Lellanova, V.G.; Uskaryov, Y. A.
PDBS Lett. 443, 348-352, 1999
A>Title: The latrophilin family: multiply spliced G protein-coupled receptors with di
A:Reference number: 218869; M0ID:99148828; PMID:10023961
A:Accession: T18391
A:Status: preliminary; translated from GB/EMBL/DBJ
A:Molecule type: mRNA
A:Residues: 1-1274 <MAT>
A:Cross-references: EMBL:AF111087; NID:g4164056; PID:g4164057; PIDN:AAD05323.1
C:Superfamily: alpha-latrotoxin receptor, calcium-independent
C:Keywords: alternative splicing; G protein-coupled receptor

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Query Match 68.4%; Score 3120.5; DB 2; Length 1274;
Best Local Similarity 93.1%; Pred. No. 2.4e-214;
Matches 608; Conservative 9; Mismatches 15; Indels 21; Gaps 3;

QY 1 AEGTRNHLNAGDITTSVRAMDQVGLLDVQLRNLTPGKDSARSLSNK----- 48
DB 576 AEGTRNHLNAGDITTSVRAMDQVGLLDVQLRNLTPGKDSARSLSNKQKRESCRAY 635
QY 49 -AMETVNNLLOPOLANARDLTTSQDLRAATMLHTVEESAFVLADNLKTDIVREND 107
DB 636 QAMETVNNLLOPOLANARDLTTSQDLRAATMLHTVEESAFVLADNLKTDIVREND 695
QY 108 NIKLEVARLSTEGNLEDLKFPEPMGHSITOLSANTLKONGRNGEIRVAFVLYNNIGPYL 167
DB 696 NIKLEVARLSTEGNLEDLKFPEPMGHSITOLSANTLKONGRNGEIRVAFVLYNNIGPYL 755
QY 168 STENASMKLGTEALSTNHSVIVNSPVITAAINKEFSNKUYLADPVVETVKHIKQSEEN 227
DB 756 STENASMKLGTEALSTNHSVIVNSPVITAAINKEFSNKUYLADPVVETVKHIKQSEEN 815
QY 228 PNCSEFSYSKRMTGYSWGCGRLTNTKTHHTSCNHLTNFAVLAHVEVKHSDAVHDL 287
DB 816 PNCSEFSYSKRMTGYSWGCGRLTNTKTHHTSCNHLTNFAVLAHVEVKHSDAVHDL 875
QY 288 LLDVITWVIGILSLVCLLCITFCFGRLOSDRNTIHNKLCISLVAELFLIGINRND 347
DB 876 LLDVITWVIGILSLVCLLCITFCFGRLOSDRNTIHNKLCISLVAELFLIGINRND 935
QY 348 OPIACAVFALLHFFELAAFTWMLFEGVOLYIMLVEFESEHSRRKXYFLVGYGMPALIV 407
DB 936 OPIACAVFALLHFFELAAFTWMLFEGVOLYIMLVEFESEHSRRKXYFLVGYGMPALIV 995
QY 408 AVSAANDYRSYGTDKVCMRLDPTFWSFICPATLIMLVIFGLALYKMFHHTAILKP 467
DB 996 AVSAANDYRSYGTDKVCMRLDPTFWSFICPATLIMLVIFGLALYKMFHHTAILKP 1055
QY 468 ESGCLDNKSWYIGAITALLCLGLTWAFLMAYINVESTVIMAYLFTFNSLQGMFIFPHC 527

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|||||
Db 1056 ESGCLDIKSWVIGALALCLLGLTMAFGMLYNESFTVIMAYLFTFINSLOGMFIFFHC 1115
QY 528 VLOKKYRKKEGKCLRTHCSCGKSTESSIGSGKTSGRTPGRYSTGSGSRIIRMMNDVVR 587
|||||
Db 1116 VLOKKYRKKEGKCLRTHCSCGKSTESSIGSGKTSGRTPGRYSTGSGSRIIRMMNDVVR 1175
QY 588 QSESSFTGDISASINREGLLNARDTSVMDTLPPLNGHG--NSYSIASGE 638
|||||
Db 1176 QSESSFTGDISASINREGMANHLSNMLRP-----HGTMNPNYNTLLGE 1222
|||||
RESULT 13
T18405
latrophilin-3, splice variant dbah, brain-specific - bovine
C:Species: Bos primigenius taurus (cattle)
C:Date: 15-Oct-1999 #sequence_revision 15-Oct-1999 #text_change 18-Feb-2000
C:Accession: T18405
R:Matsushita, H.; Leljanova, V.G.; Ushkaryov, Y.A.
FEBS Lett. 443, 348-352, 1999
A:Title: The latrophilin family: multiply spliced G protein-coupled receptors with diffe
A:Reference number: Z18869; MVID:99148828; PMID:10025961
A:Accession: T18405
A:Status: preliminary; translated from GB/EMBL/DBJ
A:Molecule type: mRNA
A:Residues: 1-1342 <MAT>
A:Cross-references: EMBL:AF11093; NID:94164068; PID:94164069; PIDN:AAD05329.1
C:Superfamily: alpha-latrototoxin receptor, calcium-independent

Query Match 68.4%; Score 3120.5; DB 2; Length 1342;
Best Local Similarity 93.1%; Pred. No. 2, 6e-214;
Matches 608; Conservative 9; Mismatches 15; Indels 21; Gaps 3;

QY 1 AEOTRNHLNAGDITTSVRAMDOLVGLLDVLRNLTPGKSDSAARSLK----- 48
Db 644 AEOTRNHLNAGDITTSVRAMDOLVGLLDVLRNLTPGKSDSAARSLKLOKRERSCAV 703
QY 49 -AMETVNNLLQPOLNAMDLTSSDQLRAATMLLTVEESAFYADNLKTDIRRENTD 107
Db 704 QAMETVNNLLQPOLNAMDLTSSDQLRAATMLLTVEESAFYADNLKTDIRRENTD 763
QY 108 NIKLEVARLSTEGNLEDLKPEKNGHSTIQLSANTLKONGRGEIVAAVLYNNLCPTL 167
Db 764 NIKLEVARLSTEGNLEDLKPEKNGHSTIQLSANTLKONGRGEIVAAVLYNNLCPTL 823
QY 168 STENASMKLCTEALSTNHSIYVNSPVTTAIIKEFSKRVYADVPVTVVHKIKOSENFN 227
Db 824 STENASMKLCTEALSTNHSIYVNSPVTTAIIKEFSKRVYADVPVTVVHKIKOSENFN 883
QY 228 PNCSEFMSYKRTMGYSTGCGRLTTNKTHTTSCNHLTNFAVLAHAEVKKHSDAVHDL 287
Db 884 PNCSEFMSYKRTMGYSTGCGRLTTNKTHTTSCNHLTNFAVLAHAEVKKHSDAVHDL 943
QY 288 LLDVITWVGILLSVCLLCIFTFECFPRGLQSDRNTIHKMLCISLFAELLFLGIRNTD 347
Db 944 LLDVITWVGILLSVCLLCIFTFECFPRGLQSDRNTIHKMLCISLFAELLFLGIRNTD 1003
QY 348 OPTACAVFALLHFFLAATFMFLVEGVOLYIMLVEFESEHSRKKFYLVGMPALIV 407
Db 1004 OPTACAVFALLHFFLAATFMFLVEGVOLYIMLVEFESEHSRKKFYLVGMPALIV 1063
QY 408 AVSAANDYRSYGTDKVCMRLDITYFIMSFIPATLIMLVIFGLALYKMFHHTALIKP 467
Db 1064 AVSAANDYRSYGTDKVCMRLDITYFIMSFIPATLIMLVIFGLALYKMFHHTALIKP 1123
QY 468 ESGCLDIKSWVIGALALCLLGLTMAFGMLYNESFTVIMAYLFTFINSLOGMFIFFHC 527
Db 1124 ESGCLDIKSWVIGALALCLLGLTMAFGMLYNESFTVIMAYLFTFINSLOGMFIFFHC 1183
QY 528 VLOKKYRKKEGKCLRTHCSCGKSTESSIGSGKTSGRTPGRYSTGSGSRIIRMMNDVVR 587
Db 1184 VLOKKYRKKEGKCLRTHCSCGKSTESSIGSGKTSGRTPGRYSTGSGSRIIRMMNDVVR 1243
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QY 588 QSESSFTGDISASINREGLLNARDTSVMDTLPPLNGHG--NSYSIASGE 638
|||||
Db 1244 QSESSFTGDISASINREGMANHLSNMLRP-----HGTMNPNYNTLLGE 1290
|||||
RESULT 14
T18390
latrophilin-3, splice variant abag, brain-specific - bovine
C:Species: Bos primigenius taurus (cattle)
C:Date: 15-Oct-1999 #sequence_revision 15-Oct-1999 #text_change 18-Feb-2000
C:Accession: T18390
R:Matsushita, H.; Leljanova, V.G.; Ushkaryov, Y.A.
FEBS Lett. 443, 348-352, 1999
A:Title: The latrophilin family: multiply spliced G protein-coupled receptors with di
A:Reference number: Z18869; MVID:99148828; PMID:10025961
A:Accession: T18390
A:Status: preliminary; translated from GB/EMBL/DBJ
A:Molecule type: mRNA
A:Residues: 1-1231 <MAT>
A:Cross-references: EMBL:AF11086; NID:94164054; PID:94164055; PIDN:AAD05322.1
C:Superfamily: alpha-latrototoxin receptor, calcium-independent
C:Keywords: alternative splicing; G protein-coupled receptor
```

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Query Match 68.4%; Score 3120; DB 2; Length 1231;
Best Local Similarity 91.8%; Pred. No. 2, 4e-214;
Matches 613; Conservative 9; Mismatches 20; Indels 26; Gaps 4;

QY 1 AEOTRNHLNAGDITTSVRAMDOLVGLLDVLRNLTPGKSDSAARSLK----- 48
Db 576 AEOTRNHLNAGDITTSVRAMDOLVGLLDVLRNLTPGKSDSAARSLKLOKRERSCAV 635
QY 49 -AMETVNNLLQPOLNAMDLTSSDQLRAATMLLTVEESAFYADNLKTDIRRENTD 107
Db 636 QAMETVNNLLQPOLNAMDLTSSDQLRAATMLLTVEESAFYADNLKTDIRRENTD 695
QY 108 NIKLEVARLSTEGNLEDLKPEKNGHSTIQLSANTLKONGRGEIVAAVLYNNLCPTL 167
Db 696 NIKLEVARLSTEGNLEDLKPEKNGHSTIQLSANTLKONGRGEIVAAVLYNNLCPTL 755
QY 168 STENASMKLCTEALSTNHSIYVNSPVTTAIIKEFSKRVYADVPVTVVHKIKOSENFN 227
Db 756 STENASMKLCTEALSTNHSIYVNSPVTTAIIKEFSKRVYADVPVTVVHKIKOSENFN 815
QY 228 PNCSEFMSYKRTMGYSTGCGRLTTNKTHTTSCNHLTNFAVLAHAEVKKHSDAVHDL 287
Db 816 PNCSEFMSYKRTMGYSTGCGRLTTNKTHTTSCNHLTNFAVLAHAEVKKHSDAVHDL 875
QY 288 LLDVITWVGILLSVCLLCIFTFECFPRGLQSDRNTIHKMLCISLFAELLFLGIRNTD 347
Db 876 LLDVITWVGILLSVCLLCIFTFECFPRGLQSDRNTIHKMLCISLFAELLFLGIRNTD 935
QY 348 OPTACAVFALLHFFLAATFMFLVEGVOLYIMLVEFESEHSRKKFYLVGMPALIV 407
Db 936 OPTACAVFALLHFFLAATFMFLVEGVOLYIMLVEFESEHSRKKFYLVGMPALIV 995
QY 408 AVSAANDYRSYGTDKVCMRLDITYFIMSFIPATLIMLVIFGLALYKMFHHTALIKP 467
Db 996 AVSAANDYRSYGTDKVCMRLDITYFIMSFIPATLIMLVIFGLALYKMFHHTALIKP 1055
QY 468 ESGCLDIKSWVIGALALCLLGLTMAFGMLYNESFTVIMAYLFTFINSLOGMFIFFHC 527
Db 1056 ESGCLDIKSWVIGALALCLLGLTMAFGMLYNESFTVIMAYLFTFINSLOGMFIFFHC 1115
QY 528 VLOKKYRKKEGKCLRTHCSCGKSTESSIGSGKTSGRTPGRYSTGSGSRIIRMMNDVVR 587
Db 1116 VLOKKYRKKEGKCLRTHCSCGKSTESSIGSGKTSGRTPGRYSTGSGSRIIRMMNDVVR 1175
QY 588 QSESSFTGDISASINREGLLNARDTSVMDTLPPLNGHGNSYASGEYSNCVOII 647
Db 1176 QSESSFTGDISASINREPY-----RETSMGVKLNT-----AYQIGASE---QCQGYK 1222
QY 648 DRGYNHNE 655
|||||
```

Db 1223 CHGYSTTE 1230

RESULT 15

T18398
latrophilin-3, splice variant bba9, brain-specific - bovine
C:Species: Bos primigenius taurus (cattle)
C:Date: 15-Oct-1999 #sequence_revision 15-Oct-1999 #text_change 18-Feb-2000
C:Accession: T18398
R:Matsushita, H.; Leljanova, V.G.; Ushkaryov, Y.A.
FEBS Lett. 443, 348-352, 1999
A:Title: The latrophilin family: multiply spliced G protein-coupled receptors with different reference number: 218869; PMID:99148828; PMID:10025961
A:Accession: T18398
A:Status: preliminary; translated from GR/EMBL/DBJ
A:Molecule type: mRNA
A:Residues: 1-1299 <MAT>
A:Cross-references: EMBL:AF111092; NID:94164066; PID:94164067; PIDN:AAD05328.1
C:Superfamily: alpha-latrotoxin receptor, calcium-independent
C:Keywords: alternative splicing; G protein-coupled receptor

Query Match 68.4%; Score 3120; DB 2; Length 1299;
Best Local Similarity 91.8%; Pred. No. 2.6e-214;
Matches 613; Conservative 9; Mismatches 20; Indels 26; Gaps 4;

```
QY 1 AEQFNHINAGDITYSVRAMQVGLLDVQLNLTPGGRKDSARSLNK----- 48
Db 644 AEQTNHINAGDITYSVRAMQVGLLDVQLNLTPGGRKDSARSLNKQKRERSGRAY 703
QY 49 -AMVETVNNLLQPOLANMRDLTSDQLRAATMLHTVEESAFVLADNLKTDIYRENTD 107
Db 704 QAMVETVNNLLQPOLANMRDLTSDQLRAATMLDYEESAFVLADNLKTDIYRENTD 763
QY 108 NIKLEVARLSTEGNEDLKFPENMGHGSTIQLSANTLKONGRNGEIRVAEVLNNLGPYL 167
Db 764 NIOLEVARLSTEGNEDLKFPENMGHGSTIQLSANTLKONGRNGEIRVAEVLNNLGPYL 823
QY 168 STENASMKLGTEALSTNHSVIVNSPVITAIINKEFSNKVYLADPVFTYKHITKOSENFN 227
Db 824 STENASMKLGTEAMSTNHSVIVNSPVITAIINKEFSNKVYLADPVFTYKHITKOSENFN 883
QY 228 PNCSEFMSYKRTMGYSTGCRLLTTHKTHHTSCNHLTNFAVLAHVEVKHSDAVHDL 287
Db 884 PNCSEFMSYKRTMGYSTGCRLLTTHKTHHTSCNHLTNFAVLAHVEVKHSDAVHDL 943
QY 288 LLDVITWVGILLICVCLLCIFTECFEFGRLQSDRNFTHKNLCISLFAELLFLGINRTD 347
Db 944 LLDVITWVGILLICVCLLCIFTECFEFGRLQSDRNFTHKNLCISLFAELLFLGINRTD 1003
QY 348 QPIACAVFAALLHFFFLAFTMFLFEGVQLYIMLVEFESEHSRRKRYLVGYGMPALIV 407
Db 1004 QPIACAVFAALLHFFFLAFTMFLFEGVQLYIMLVEFESEHSRRKRYLVGYGMPALIV 1063
QY 408 AVSAADVRSYGTDKVCMRLDITYMSFTGPATLIMLVFIIGALYKMFHHTAILKP 467
Db 1064 AVSAADVRSYGTDKVCMRLDITYMSFTGPATLIMLVFIIGALYKMFHHTAILKP 1123
QY 468 ESGCLINIKSWVIGAILLCLGLTMAFGMLYINESTVIMAYLFTIFNSLQGMFIFIFHC 527
Db 1124 ESGCLINIKSWVIGAILLCLGLTMAFGMLYINESTVIMAYLFTIFNSLQGMFIFIFHC 1183
QY 528 VLQKKVREYEGKCLRTGCCSGKSTSSIGSGKTSRTPGRYSTGQSQRIRRMNDYVRK 587
Db 1184 VLQKKVREYEGKCLRTGCCSGKSTSSIGSGKTSRTPGRYSTGQSQRIRRMNDYVRK 1243
QY 588 QSESEFTIGDINSASLREGILLNNAADTSVMDTLPLNGHNGNSYIASGEYLSNCYQII 647
Db 1244 QSESEFTIGDINSASLREPI-----RETSMSGVKLNI-----AYQIGASE---QCQGYK 1290
QY 648 DRGYNHNE 655
Db 1291 CHGYSTTE 1298
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Search completed: December 10, 2002, 11:13:10
Job time : 46 secs

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GenCore version 5.1.3
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OM protein - protein search, using sw model

Run on: December 10, 2002, 10:57:49 ; Search time 15 Seconds
(without alignments)
2411.157 Million cell updates/sec

Title: US-09-744-226A-1
4563
Sequence: 1 AECTRNHLNMGDIRYSVRAM.....KDGTPPGSSSKGAHLVTSLSL 872

Scoring table: BLOSUM62
Gapop 10.0 , Gapext 0.5

Searched: 112892 seqs, 41476328 residues

Total number of hits satisfying chosen parameters: 112892

Minimum DB seq length: 0
Maximum DB seq length: 2000000000

Post-processing: Minimum Match 0%
Maximum Match 100%
Listing first 45 summaries

Database : SwissProt.40:*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	Query Match	Length	ID	Description
1	762	16.7	835	1 CD97_HUMAN	P48960 homo sapien
2	749.5	16.4	931	1 EMRI1_MOUSE	O61549 mus musculu
3	715.5	15.7	886	1 EMRI1_HUMAN	O14246 homo sapien
4	700.5	15.4	3034	1 CLRL_MOUSE	O35161 mus musculu
5	692	15.2	3014	1 CLRL_HUMAN	O90966 homo sapien
6	637.5	14.0	2144	1 CLR2_RAT	O99492 rattus norv
7	636.5	13.9	2923	1 CLR2_HUMAN	O99494 homo sapien
8	623.5	13.7	2920	1 CLR2_MOUSE	O97080 mus musculu
9	578.5	12.7	1522	1 BAI3_HUMAN	O60242 homo sapien
10	520	11.4	3313	1 CLR3_RAT	O88278 rattus norv
11	518.5	11.4	3301	1 CLR3_MOUSE	O91210 mus musculu
12	507.5	11.1	3312	1 CLR3_HUMAN	O90997 homo sapien
13	505.5	11.1	1572	1 BAI2_HUMAN	O60241 homo sapien
14	496.5	10.9	1584	1 BAI1_HUMAN	O14514 homo sapien
15	483	10.6	3579	1 STAN_DROME	O94588 drosophila
16	302	6.6	441	1 DIHR_ACHDO	O16983 acheta dome
17	290.5	6.4	415	1 CRF1_MOUSE	P35347 mus musculu
18	290.5	6.4	415	1 CRF1_RAT	P35353 rattus norv
19	279.5	6.1	415	1 CRF1_SHEEP	O62772 ovis aries
20	273	6.0	444	1 CRF1_HUMAN	P34598 homo sapien
21	270.5	5.9	420	1 CRF1_CHICK	O90812 gallus gall
22	268	5.9	413	1 CRF2_XENLA	O46603 xenopus lae
23	261.5	5.7	431	1 CRF2_MOUSE	O60748 mus musculu
24	260.5	5.7	411	1 CRF2_RAT	P47866 rattus norv
25	256	5.6	395	1 DIHR_MANSE	P33464 menduca sex
26	250.5	5.5	415	1 CRF1_XENLA	O46602 xenopus lae
27	245.5	5.4	466	1 GIPR_HUMAN	P45546 homo sapien
28	241.5	5.3	468	1 PACR_HUMAN	P41586 homo sapien
29	240	5.3	461	1 CGRR_HUMAN	O16602 homo sapien
30	238.5	5.2	496	1 PACR_MOUSE	P70205 mus musculu
31	238.5	5.2	411	1 CRF2_HUMAN	O13324 homo sapien
32	238.5	5.2	513	1 PACR_BOVIN	O29627 bos taurus
33	237	5.2	489	1 GLP1_MOUSE	O35659 mus musculu

34	236	5.2	464	1	CGRR_RAT	O63118 rattus norv
35	235	5.2	478	1	CALR_CAVPO	O08893 cavia porce
36	231.5	5.1	455	1	GIPR_RAT	P43219 rattus norv
37	230	5.0	445	1	SCRC_RABIT	O46502 oryctolagus
38	228	5.0	440	1	SCRC_HUMAN	P47872 homo sapien
39	225	4.9	457	1	VIPR_HUMAN	P32241 homo sapien
40	225	4.9	459	1	PTRR_MOUSE	P41593 mus musculu
41	224.5	4.9	449	1	SCRC_RAT	P23811 rattus norv
42	223.5	4.9	463	1	GLP1_RAT	P32301 rattus norv
43	223	4.9	490	1	CALR_HUMAN	P30988 homo sapien
44	223	4.9	644	1	Y044_CAEEL	O09460 caenorhabd1
45	222.5	4.9	463	1	GLP1_HUMAN	P43220 homo sapien

ALIGNMENTS

```

RESULT 1
CD97_HUMAN          STANDARD:      PRT:      835 AA.
ID   CD97_HUMAN
AC   P48960:
DT   01-FEB-1996 (Rel. 33, Created)
DT   30-MAY-2000 (Rel. 39, Last sequence update)
DT   15-JUN-2002 (Rel. 41, Last annotation update)
DE   Leucocyte antigen CD97 precursor.
GN   CD97.
OS   Homo sapiens (Human).
OC   Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC   Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
OX   NCBI_Taxid=9606;
RN   [1]
RP   MEDLINE=95363161; PubMed=7636245;
RA   Hamann J., Eichler W., Hamann D., Kerstens H.M.J., Poddighe P.J.,
RA   Hoovers J.M.N., Hartmann J.M., Straus M., van Lier R.A.W.;
RT   "Expression cloning and chromosomal mapping of the leukocyte
RT   activation antigen CD97, a new seven-span transmembrane molecule of
RT   the secretin receptor superfamily with an unusual extracellular
RT   domain.";
RL   J. Immunol. 155:1942-1950(1995).
RN   [2]
RP   SEQUENCE FROM N.A.
RP   TISSUE=Fore skin;
RX   MEDLINE=96230339; PubMed=8786105;
RA   Hamann J., Hartmann B., van Lier R.A.W.;
RT   "Structure of the human CD97 gene: exon shuffling has generated a new
RT   type of seven-span transmembrane molecule related to the secretin
RT   receptor superfamily.";
RL   Genomics 32:144-147(1996).
RN   [3]
RP   REVISIONS.
RA   Hamann J.;
RL   Submitted (OCT-1997) to the EMBL/GenBank/DBJ databases.
CC   -!- FUNCTION: COULD BE A RECEPTOR POTENTIALLY INVOLVED IN BOTH
CC   ADHESION AND SIGNALING PROCESSES EARLY AFTER LEUKOCYTE ACTIVATION.
CC   -!- SUBCELLULAR LOCATION: Integral membrane protein.
CC   -!- SIMILARITY: CONTAINS 5 EGF-LIKE DOMAINS.
CC   -!- SIMILARITY: BELONGS TO FAMILY 2 OF G-PROTEIN COUPLED RECEPTORS.
CC   -!- SIMILARITY: CONTAINS 1 GPS DOMAIN.
CC   -!- DATABASE: NAME=PROV; NOTE=CD guide CD97 entry;
CC   WWW="http://www.ncbi.nlm.nih.gov/prov/cd/cd97.htm".
CC   -----
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CC   entities requires a license agreement (see http://www.isb-sdb.ch/announce/
CC   or send an email to license@isb-sdb.ch).
CC   -----
CC   EMBL: X84700; CAA59173.1;
CC   EMBL: X94630; CAA64333.1;
CC   EMBL: X94631; CAA64333.1; JOINED.

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FT	DISULFID	171	186		BY SIMILARITY.
FT	DISULFID	188	207		BY SIMILARITY.
FT	DISULFID	213	226		BY SIMILARITY.
FT	DISULFID	220	235		BY SIMILARITY.
FT	DISULFID	237	256		BY SIMILARITY.
FT	CARBOHYD	333	333		N-LINKED (GLCNAC. . .)
FT	CARBOHYD	338	38		(POTENTIAL.)
FT	CARBOHYD	108	108		N-LINKED (GLCNAC. . .)
FT	CARBOHYD	371	203		(POTENTIAL.)
FT	CARBOHYD	371	371		N-LINKED (GLCNAC. . .)
FT	CARBOHYD	416	406		(POTENTIAL.)
FT	CARBOHYD	413	413		N-LINKED (GLCNAC. . .)
FT	CARBOHYD	453	453		(POTENTIAL.)
FT	CARBOHYD	520	520		N-LINKED (GLCNAC. . .)
FT	CONFLICT	121	213		(POTENTIAL.)
SQ	SEQUENCE	835 AA;	91941 MW;	050672E7A4C12A9E CRC64;	
<hr/>					
Query Match 16.7%; Score 762; DB 1; Length 835;					
Best local Similarity 32.9%; Pred. No. 6,1e-42;					
Matches 189; Conservative 108; Mismatches 213; Indels 64; Gaps 18;					
OY	30 QLRNLTPGKDSARSLSNKAVETVNNLQ-PQLANWRDLTTSDDLRAATMLHTFYES 88				
Db	281 KYQDLGRSKSTSSAEVTIQNIYKLVDLEMAPGDVEA--LAPVRHLIATOLLNLEDI 337				
OY	89 AFVLADNLKTDIYRENTDNIKELVARLTSGCNLEDLKFPEMNGH-STIQLSANTLKON 147				
Db	338 MRLLAKSLPKRPFTYISPSNTETL-MOERGD-----KNVTGGOSARRKKLMWAVA 389				
OY	148 GRN--GEIRVAFLVLYNNGPYLSTENASMKGTALSTNSHYVNSPYI-----TAAI 198				
Db	390 GAEDPPPAVGILSIQNMTTLA--NSLNHSKKQALEETIESS--TRGYQLRLSAY 445				
OY	199 NKFE---SNKYLLADPVVFVKHKIKOSE-----ENFPN-----CSFWYSKRRTM 240				
Db	446 NSIFLSHNNTKELMSPLFAFSHLESDDGEAGRDPAADVMPGROELLCAFMK-SDSR 504				
OY	241 TGVYSTOGCRLLTNKTHHTTSCNHLTFEAVLMAHEVYKSHSDAHDLLDYITWGILLS 300				
Db	505 GGHMATEVCQYLGSKNGSTGCCSHLSSEFTIMAHAYDE-----DMKLTITRVGLALS 558				
OY	301 LVCLLICITCFPCFRGLQSDRNITHKNICISLFVAELLFLGINRTDPPIA--CAVPAA 358				
Db	559 LFCCLLCITFLVLPRIQGSRTTIHLHCICLFEGSTTEFLGIENGGVOGLRCRLVAGL 618				
OY	359 LHFFFLAFTMPFLLEGVOLYIMLVEVEFSEHSRRKYFYLVGCGMPALIVAAVAADVRSY 418				
Db	619 LHYCFLLAFCMSSLEGLELTVLVYRVROGOOLSTRMCLIGCYVPLLIVGSAALYSNGY 678				
OY	419 GTDCWCWLRLDTYTFWSFIGPATLIIMLVIFLGIALYKMFHHRAILKPESGCLDNIKSW 478				
Db	679 GRPRYCWMDFRGFLMSPLGVPTEFLICNAVIAFYVTWKLIKQKSEINPMDKMLKKARAL 738				
OY	479 VIGAILALLCILGITWARGLAMINESTVMALFTIPNSLOGMFIIFICYQAKVRYKG 538				
Db	739 TITFAIOFLFLLGCWTWEGLETFDDRSLVLTFTVINLLOGAFLYILHCLLNKKVREEYR 798				
OY	539 K--CLRTHCCSGK-----STESSIGSGKTSGSR 564				
Db	799 KWACL---VAGGSKYSEPTSTTGTHNQTYALR 829				
<hr/>					
RESULT 2					
ID	EMRL_MOUSE	STANDARD:	PRT:	931 AA.	
AC	Q61349;				
DT	01-NOV-1997 (Rel. 35, Created)				
DT	01-NOV-1997 (Rel. 35, Last sequence update)				
DT	15-JUN-2002 (Rel. 41, last annotation update)				
DE	Cell surface glycoprotein EMRL precursor (EMRL hormone receptor) (cell surface glycoprotein P4/80).				
OS	Mus musculus (Mouse).				

OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
 OC Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Mus.
 OX NCBI_TaxID=10090;
 RN [1]
 RP SEQUENCE FROM N.A.
 RC STRAIN=BALE/c; TISSUE=Peritoneal cavity;
 RX MEDLINE=96132946; PubMed=8550607;
 RA McKnight A.J., Macfarlane A.J., Drl P., Turley L., Willis A.C.,
 RA Gordon S.;
 RT "Molecular cloning of F4/80, a murine macrophage-restricted cell
 RT surface glycoprotein with homology to the G-protein-linked
 RT transmembrane 7 hormone receptor family";
 RL J. Biol. Chem. 271:486-489(1996).
 RN [2]
 RP SEQUENCE FROM N.A.
 RX MEDLINE=97312684; PubMed=9169125;
 RA Lin H.H., Stubbs L.J., Mucenski M.L.;
 RT "Identification and characterization of a seven transmembrane hormone
 RT receptor using differential display.";
 RL Genomics 41:301-308(1997).
 CC -!- FUNCTION: PROBABLY INVOLVED IN CELL ADHESION WITHIN TISSUES
 CC AND RECEPTOR SIGNALING.
 CC -!- SUBCELLULAR LOCATION: Integral membrane protein.
 CC -!- TISSUE SPECIFICITY: IN MACROPHAGES; BUT ABSENT FROM THOSE WHICH
 CC ARE LOCALIZED WITHIN T-CELL AREAS OF LYMPH NODES AND SPLEEN.
 CC LOW LEVEL OF EXPRESSION ON BLOOD MONOCYTES.
 CC -!- SIMILARITY: CONTAINS 7 EGF-LIKE DOMAINS.
 CC -!- SIMILARITY: BELONGS TO FAMILY 2 OF G-PROTEIN COUPLED RECEPTORS.
 CC -!- SIMILARITY: CONTAINS 1 GPS DOMAIN.
 CC -----
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 CC -----
 DR EMBL: X93328; CAA63720.1; -
 DR EMBL: U66888; AAC53184.1; -
 DR HSP: P35555; IEMN.
 DR MGD: MGI:106912; Emr1.
 DR InterPro: IPR000152; Asx_hydroxyl.
 DR InterPro: IPR000561; EGF-like.
 DR InterPro: IPR001881; EGF Ca.
 DR InterPro: IPR000832; GPCR_secretin.
 DR InterPro: IPR000203; PKD_cys-rich.
 DR Pfam: PF00002; 7tm_2; 1.
 DR Pfam: PF00008; EGF; 6.
 DR Pfam: PF01825; GPS; 1.
 DR SMART: SM00179; EGF_CA; 6.
 DR SMART: SM00001; EGF_Like; 1.
 DR SMART: SM00303; GPS; 1.
 DR PROSITE: PS00010; ASX_HYDROXYL; 6.
 DR PROSITE: PS01186; EGF_2; 1.
 DR PROSITE: PS01187; EGF_CA; 5.
 DR PROSITE: PS50221; GPS; 1.
 DR PROSITE: PS00650; G_PROTEIN_RECP_F2_2; 1.
 DR PROSITE: PS50261; G_PROTEIN_RECP_F2_4; 1.
 DR G-protein coupled receptor; Transmembrane; Receptor; Glycoprotein;
 KW EGF-like domain; Repeat; Signal.
 FT SIGNAL 1 27
 FT CHAIN 1 931
 FT DOMAIN 28 644
 FT TRANSMEM 645 672
 FT DOMAIN 673 679
 FT TRANSMEM 680 701
 FT DOMAIN 702 711
 FT TRANSMEM 712 735
 FT DOMAIN 736 754
 FT TRANSMEM 755 776
 FT DOMAIN 777 792
 FT TRANSMEM 793 821
 FT TRANSMEM
 POTENTIAL.
 CELL SURFACE GLYCOPROTEIN EMBL.
 EXTRACELLULAR (POTENTIAL).
 POTENTIAL.
 CYTOPLASMIC (POTENTIAL).
 POTENTIAL.
 EXTRACELLULAR (POTENTIAL).
 POTENTIAL.
 CYTOPLASMIC (POTENTIAL).
 POTENTIAL.
 CYTOPLASMIC (POTENTIAL).
 POTENTIAL.
 EXTRACELLULAR (POTENTIAL).
 POTENTIAL.
 CYTOPLASMIC (POTENTIAL).
 POTENTIAL.
 EXTRACELLULAR (POTENTIAL).
 POTENTIAL.

FT DOMAIN 822 839
 FT TRANSMEM 840 859
 FT DOMAIN 860 874
 FT TRANSMEM 875 897
 FT DOMAIN 898 931
 FT DOMAIN 932 80
 FT DOMAIN 131 132
 FT DOMAIN 133 172
 FT DOMAIN 173 221
 FT DOMAIN 222 271
 FT DOMAIN 272 318
 FT DOMAIN 319 367
 FT DOMAIN 367 641
 FT SITE 506 508
 FT DISULFID 36 48
 FT DISULFID 42 57
 FT DISULFID 59 79
 FT DISULFID 85 98
 FT DISULFID 92 107
 FT DISULFID 109 131
 FT DISULFID 137 149
 FT DISULFID 143 158
 FT DISULFID 160 171
 FT DISULFID 177 189
 FT DISULFID 183 198
 FT DISULFID 200 220
 FT DISULFID 226 239
 FT DISULFID 233 248
 FT DISULFID 250 270
 FT DISULFID 276 286
 FT DISULFID 280 295
 FT DISULFID 297 317
 FT DISULFID 323 336
 FT DISULFID 347 366
 FT DISULFID 148 148
 FT CARBOHYD 167 167
 FT CARBOHYD 229 229
 FT CARBOHYD 259 269
 FT CARBOHYD 283 283
 FT CARBOHYD 405 405
 FT CARBOHYD 417 417
 FT CARBOHYD 474 474
 FT CARBOHYD 498 498
 FT CARBOHYD 706 706
 SQ SEQUENCE 931 AA; 102129 MW; 52963A667E8B76B5 CRC64;
 Query Match 16.4%; Score 749.5; DB 1; Length 931;
 Best Local Similarity 31.9%; Pred. No. 4, 7e-41;
 Matches 176; Conservative 101; Mismatches 230; Indels 45; Gaps 11;
 QY 26 LLDVQLRLTL-PEGKDSAAARSLKNAVEFVNNILQPOLANMRDLTTSQRLAATMLHT 84
 DB 410 ILDNFCNKSAFVSLQSAATSV-----SLVLEQDA-TTWEELSKERTSTGLTLLT 459
 QY 85 VEEASFAVLNDNLKTDIVENDTNIKLEVARLSTEGNLDLKRPEN-----MGHGSTIOL 139
 DB 460 VEST-----MVALILITSGNASQMTQTEYLDIESKVLNEEKENESINLAARGDKMAY 512
 QY 140 SANTLQNGRNGERIRVAFVLYNNIGPLYSTENASMKLTGEALSTNNSVIVNSPITAAIN 199
 DB 513 GCFITKESYSTAGPVAFAFSAFAMESVULNDRFEDQSPFKLIMNSRYV--GGTVGEEK 570
 QY 200 KEFSNMYVLADPVFTVFKHKQSEENFNRCSSWTSKRTMGYSWGCRLLTTKKTIT 259
 DB 571 EDPSK-----PIYTLQHIQPKQKSERPICVSWND--VEDGRMPSCCEIVEASETH 622
 QY 260 TGSCHNLTPNAVYMAHVEYKHSADVADHLLDVTWGGILSLVCLICLFTPCFFGLQS 319
 DB 623 VCSCHNMANLITMASGEL-----TWEFSLYISHGVYISLVCALAIAITFLCAVON 677
 QY 320 DRNTIKNLICISLFAVELFLGINTDPIACAVFAALHFFFLAFTMPELEGVQLYI 379
 DB 320 DRNTIKNLICISLFAVELFLGINTDPIACAVFAALHFFFLAFTMPELEGVQLYI 379

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Db 678 HNTVHMLHCVCOLFLAKLIEFLTGIDKTDQNTQCAIIAGLHFLHFLACFPFMMLEAVEMLEL 737
OY 380 M-----LVEVESEHSRRKRYFLVGYGMPALIVAVSAADYRSYGTDRKVCMLRLDTYFTW 434
Db 738 MYRNLKVVNYVESRRNIKMKMLHCAFGYGLFPLVLIIVISASVQPRGYGHNRNCMLNTEGTFTW 797
OY 435 SPICGATLILIMNVFLGLALCKMHHHTAILKPESSGCLDNISWVIGATALLCLGLTWA 494
Db 798 SFLGSPVCMTITINSVLLMTWLTMLVOKLCSVSSEVSKIKDFTLLFPKALTAQIFILGCSNV 857
OY 495 FGLMIVNESTVYMAVLFTIFNSLQGMFFIFHCYLOKRVKREYGCCL--RTHCCSGKSTP 552
Db 858 LGIFQIGPLASIMAVLFTIINSLQGAFFILHICLNLRQVREDEKLLTKTKLDLSHSQTS 917
OY 553 SSISGKTSJGSR 564
Db 918 GILLSMPTSTK 929

RESULT 3
EMRL_HUMAN STANDARD: PRT: 886 AA.
ID EMRL_HUMAN
AC 014246:
DT 01-NOV-1997 (Rel. 35, Created)
DT 01-NOV-1997 (Rel. 35, Last sequence update)
DT 15-JUN-2002 (Rel. 41, Last annotation update)
DE Cell surface glycoprotein EMRL precursor (EMRL hormone receptor).
GN EMRL.
OS Homo sapiens (Human).
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC Mammalia; Eutheria; Primates; Catarrhini; Hominiidae; Homo.
OX NCBI_TaxID=9606;
RN (1)
RP SEQUENCE FROM N.A.
RX MEDLINE=95324926; PubMed=7601460;
RA Band V., Chisoe S.L., Viegas-Pequignot E., Diliong S., N'Guyen V.C.,
RA Roe B.A., Lipinski M.;
RT "EMRL, an unusual member in the family of hormone receptors with
RT seven transmembrane segments.";
RL Genomics 26:334-344(1995).
CC -1- FUNCTION: PROBABLY INVOLVED IN CELLULAR RESPONSE TO A HORMONE OR
CC AN INTERACTION WITH A PROTEIN LIGAND.
CC -1- SUBCELLULAR LOCATION: Integral membrane protein.
CC -1- TISSUE SPECIFICITY: WIDE EXPRESSION; INCREASED LEVELS IN
CC PERIPHERAL BLOOD MONONUCLEAR CELLS.
CC -1- PTM: N- AND O-GLYCOSYLATED; (POSSIBLE).
CC -1- SIMILARITY: CONTAINS 6 EGF-LIKE DOMAINS.
CC -1- SIMILARITY: BELONGS TO FAMILY 2 OF G-PROTEIN COUPLED RECEPTORS.
CC -1- SIMILARITY: CONTAINS 1 GPS DOMAIN.
CC -----
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CC -----
DR EMBL: X81479; CAA57232.1; -.
DR HSSP: P00736; IAPQ.
DR Genew: HGNC:3336; EMRL.
DR MIM: 600493; -.
DR InterPro: IPR000152; Asx_hydroxyl.
DR InterPro: IPR000561; EGF-like.
DR InterPro: IPR001881; EGF-like.
DR InterPro: IPR000832; GPCR_secretin.
DR InterPro: IPR000203; PKD_cys-rich.
DR Pfam: PF00002; 7tm_2; 1.
DR Pfam: PF00008; EGF; 5.
DR Pfam: PF01825; GPS; 1.
DR SMART: SM00179; EGF_CA; 5.
DR SMART: SM00001; EGF_like; 1.
DR SMART: SM00303; GPS; 1.

```

DB	Query Match	Best Local Similarity	Matches	Conservative	Indels	Gaps
DR	PROSITE: PS01186; ASX_HYDROXYL. 6.	15.7%;	Score 715.5;	DB 1;	Length 886;	
DR	PROSITE: PS01187; EGF_CA. 5.	30.4%;	Pred. No. 7.1e-39;			
DR	PROSITE: PS00221; GPs. 1.					
DR	PROSITE: PS00650; G_PROTEIN_RECIP_F2_2; 1.					
DR	PROSITE: PS00261; G_PROTEIN_RECIP_F2_4; 1.					
KM	G-protein coupled receptor; Transmembrane; Receptor; Glycoprotein;					
KM	EGF-like domain; Repeat; Signal.					
FT	SIGNAL	1	17			
FT	CHAIN	18	886			
FT	DOMAIN	18	599			
FT	TRANSMEM	600	627			
FT	DOMAIN	628	634			
FT	TRANSMEM	635	656			
FT	DOMAIN	657	666			
FT	TRANSMEM	667	690			
FT	DOMAIN	691	709			
FT	TRANSMEM	710	731			
FT	DOMAIN	732	747			
FT	TRANSMEM	748	776			
FT	DOMAIN	777	794			
FT	TRANSMEM	795	814			
FT	DOMAIN	815	829			
FT	TRANSMEM	830	852			
FT	DOMAIN	853	866			
FT	DOMAIN	31	79			
FT	DOMAIN	80	131			
FT	DOMAIN	132	171			
FT	DOMAIN	172	213			
FT	DOMAIN	221	267			
FT	DOMAIN	268	316			
FT	DOMAIN	547	596			
FT	DOMAIN	317	599			
FT	DISULFID	35	47			
FT	DISULFID	41	56			
FT	DISULFID	58	78			
FT	DISULFID	84	97			
FT	DISULFID	91	106			
FT	DISULFID	108	130			
FT	DISULFID	136	148			
FT	DISULFID	142	157			
FT	DISULFID	159	170			
FT	DISULFID	176	188			
FT	DISULFID	182	197			
FT	DISULFID	199	212			
FT	DISULFID	225	235			
FT	DISULFID	229	244			
FT	DISULFID	246	266			
FT	DISULFID	272	285			
FT	DISULFID	279	294			
FT	DISULFID	296	315			
FT	CARBOHYD	94	94			
FT	CARBOHYD	99	99			
FT	CARBOHYD	127	127			
FT	CARBOHYD	167	167			
FT	CARBOHYD	189	189			
FT	CARBOHYD	194	194			
FT	CARBOHYD	232	232			
FT	CARBOHYD	258	258			
FT	CARBOHYD	312	312			
FT	CARBOHYD	366	366			
FT	CARBOHYD	375	375			
FT	CARBOHYD	448	448			
FT	CARBOHYD	661	661			
SEQ	SEQUENCE	886 AA:	97680 MW;	7456CA56FB624D99	CRC64;	
QY	47 NKAMVETVNNLLDP-----QALNANRDLTTSQQLRAATMLHTFVEBSAFVLAD-----NLL 97	15.7%;	Score 715.5;	DB 1;	Length 886;	
DB	366 NKTVTVAISLKTETSEVPVYLKQITSMNTKTFKEETSSLATFLEVSVE--SMTLASFWKPSAN 423					

FT	CARBOHYD	793	793	N-LINKED	(GLCNAC . .)	(POTENTIAL)
FT	CARBOHYD	1129	1129	N-LINKED	(GLCNAC . .)	(POTENTIAL)
FT	CARBOHYD	1154	1154	N-LINKED	(GLCNAC . .)	(POTENTIAL)
FT	CARBOHYD	1228	1228	N-LINKED	(GLCNAC . .)	(POTENTIAL)
FT	CARBOHYD	1264	1264	N-LINKED	(GLCNAC . .)	(POTENTIAL)
FT	CARBOHYD	1274	1274	N-LINKED	(GLCNAC . .)	(POTENTIAL)
FT	CARBOHYD	1302	1302	N-LINKED	(GLCNAC . .)	(POTENTIAL)
FT	CARBOHYD	1591	1591	N-LINKED	(GLCNAC . .)	(POTENTIAL)
FT	CARBOHYD	1638	1638	N-LINKED	(GLCNAC . .)	(POTENTIAL)
FT	CARBOHYD	1655	1655	N-LINKED	(GLCNAC . .)	(POTENTIAL)
FT	CARBOHYD	1994	1994	N-LINKED	(GLCNAC . .)	(POTENTIAL)
FT	CARBOHYD	2118	2118	N-LINKED	(GLCNAC . .)	(POTENTIAL)
FT	CARBOHYD	2137	2137	N-LINKED	(GLCNAC . .)	(POTENTIAL)
FT	CARBOHYD	2144	2144	N-LINKED	(GLCNAC . .)	(POTENTIAL)
FT	CARBOHYD	2155	2155	N-LINKED	(GLCNAC . .)	(POTENTIAL)
FT	CARBOHYD	2160	2160	N-LINKED	(GLCNAC . .)	(POTENTIAL)
FT	CARBOHYD	2272	2272	N-LINKED	(GLCNAC . .)	(POTENTIAL)
FT	CARBOHYD	2430	2430	N-LINKED	(GLCNAC . .)	(POTENTIAL)
FT	CARBOHYD	2452	2452	N-LINKED	(GLCNAC . .)	(POTENTIAL)
FT	CARBOHYD	2538	2538	N-LINKED	(GLCNAC . .)	(POTENTIAL)
SQ	SEQUENCE	3034 AA:	330477 MW:	EPF38180AF5ED8A8	CRC64:	
Query Match						
Best Local Similarity		15.4%	Score 700.5:	DB 1:	Length 3034:	
Matches 237:		Conservative 166:	Mismatches 356:	Indels 207:	Gaps	
QY	1 AEOTNHLNADITY--SVRAMDVLGLDVLQVLRNLTGGKDSAAKSLN-KAMETVYNN	56				
DB	2150 AKALRNATNGSSTLFQNDVRAVQOLLARI-LQHESNQGGDLATPEANFHEDVYHTSA	2208				
QY	57 LIQPOLANWRDLTTSQDLRAATMLH-----TVESAFVLADNLKTDI	101				
DB	2209 LLAPEATSEWQIORS-EAGAAQLRHFEEAFGSNVAARNVKRTYLRPFVIVTANMILAVDI	2267				
QY	102 VRE-----NNDINKLEVAR---LSTGNLDELKPENNMGHSTIDL-----	139				
DB	2268 FDKLFTGCAQVPREDDIQEELPRELESSVSPADTKRPBKPK-EGGVVALITNRRTPLTA	2322				
QY	140-----SANTLKONGNCEIRPAF-VLYNNNGPYL---STENAMKLGTEALST	183				
DB	2327 QPEPAKEHETSSSRNRHNPDEQGFANALVIVIRITGOLLPRHEDDHSLSLPRP---	2383				
QY	184 NHSVIVNSPVITAAINKFSKKVYLADEVVITYKHKIKOSEBENPNPCSWSYSKRT-MTG	242				
DB	2384-----VINPVPVSAVWYSEGRPLPSSLDORPLVFEFSLTEEBERSKPCVCFPMNHSIDTGGTG	2439				
QY	243 YWSTQGGCLLTNTKTHNTTCSGNHLTNAVILMAHANEVCKHSDAVHDLDDIIVTWGILLSLV	302				
DB	2440 GMSAGGCELLSRNTHVATCCSHASCAVLMDISRREHGV--LPLKITYTAALSLSV	2496				
QY	303 CLTICIEFFCFEPLQSDRMTIHKNLICISLFVALLFLGINRTDPICAVFAALLHFF	362				
DB	2497 ALLVAFVLLSLVRLRSLNLSIHKNLIALAFESQDLIFPMWGINGTEPRFLCTYVALLHNV	2556				
QY	363 FLAAFTWMELEGVOLYIMLVEFESEHSRRKRYLVGQGNPALIYAASVAVDYRSYGTDK	422				
DB	2557 SMGFTFAMTLVENLHVRYMLTEVRNIDGPRFHVHVGWGIPTALVIGLADLPQGYGMD	2618				
QY	423 VCVRLRDIFYFIRWSTIGPATILIMN-VIPL---GIALYKMFHHTALRKESCDLNIKSM	478				
DB	2617 FCMVSLDQTLTSLSPAGVPGVGIIVIIIVYIFLASKVSCQRKHN---YERKGVSMLEP-	2671				
QY	479 VIGALIALCLLGLFWAGFLWYNESFVIMAYLETINSLOGMFIFFHVLQKKVREK-	537				
DB	2672---AFLLILLYTATWILGLLAVNSDITLSPHYLRPAASCIDGIFVLLPHCVAHREVRKHLR	2722				
QY	538---GKCLRTCHCSGKSGTSISGKTSGRTPRGARYSTGSQSHIRRMNDYIRKOSSESF	593				
DB	2729 AVLAGKKQLQD--DSATVTRATLTLLRSLNCNT---YSEGP-----DMLR-----	2767				
QY	594 ITGDINSASLSNREGCLNNARDTSY---MDTLPNGNHNSTYASGELYSNCVQIIDR	649				
DB	2768 -TALGESPATID-----STTRDEGVOKLVSYPSPAGNNGEPT-----SFIRNSKK	2814				

QY 650 GYNHETALEKKIKELASNYIPSYLNNHRSSEONRLMN-----KLVNVL 696
 Db 2815 ANGPDSSELSLDEHSSSVASHTSDSEDDGEAEKMNAGPAHSTPKADALANIV 2874
 QY 697 GSGREDDAIVLDATSFNHEESLGLEL-----IHE-----ESPAPLLPPRV 737
 Db 2875 PAGWDESLAGSDSELDTEPHIKVETKVSVELHROAGNHCGRPSDESVLAKPVAV 2934
 QY 738 YSTEMNHPHHTRRRIPOHSESF-----PLLT--NHTEDLOSPPHDSLY 782
 Db 2935 LSSQ-----PDEORGIILKNKYTPPPLPEOPLKSLRLKRLADCCOSPTSSPT 2982
 QY 783 TSMPTLACVAATESYTT--STOTEPPEAKCAEDVYKSMPTNLSRNHVOLHTYYOLG 840
 Db 2983 SSLSGDDGVHATDCVITITKTRREP-----GREHLNGLVAMNVRIG 3022
 QY 841 RGSSDG 846
 Db 3023 SQAANG 3028

RESULT 5
 CLRL_HUMAN STANDARD; PRT; 3014 AA.
 AC Q9NYO6; Q9Y526; Q9Y506; Q9Y722; Q9BMO5;
 DT 15-JUN-2002 (Rel. 41, Created)
 DT 15-JUN-2002 (Rel. 41, Last sequence update)
 DE Caderlin EGF LAG seven-pass G-type receptor 1 precursor (Flamingo
 homolog 2) (hml2).
 GN CELSRL OR CDHP9 OR FM12.
 OS Homo sapiens (Human).
 OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
 OC Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
 OX NCBI_TaxId=9606;
 RN [1]
 RP SEQUENCE FROM N.A.
 RX MEDLINE=20202599; PubMed=10716726;
 RA Wu Q., Maniatis T.,
 RT "Large exons encoding multiple ectodomains are a characteristic
 RL feature of protocadherin genes";
 RL Proc. Natl. Acad. Sci. U.S.A. 97:3124-3129(2000).
 RN [2]
 RP SEQUENCE FROM N.A.
 RX MEDLINE=20057165; PubMed=10591208;
 RA Dunham I., Hunt A.R., Collins J.E., Bruskiwich R., Beare D.M.,
 RA Clamp M., Smitk L.J., Alnsough R., Almeida J.P., Babbage A.K.,
 RA Baguley C., Bailey J., Barlow K.F., Bates K.N., Beasley O.P.,
 RA Bird C.P., Blakey S.E., Bridgeman A.M., Buck D., Burgess J.,
 RA Burrill W.D., Burton J., Carder C., Carter N.P., Chen Y., Clark G.,
 RA Clegg S.M., Cobley V.E., Cole C.G., Collier R.E., Connor R.,
 RA Conroy D., Corby N.R., Coville G.J., Cox A.V., Davys J., Dawson E.,
 RA Dhami P.D., Dockree C., Dodsorth S.J., Durbin R.M., Ellington A.G.,
 RA Evans K.L., Fey J.M., Fleming K., French L., Garner A.A.,
 RA Gilbert J.G.R., Goward M.E., Grafham D.V., Griffiths M.N.D., Hall C.,
 RA Hall R.E., Hall-Tamlyn G., Heathcote R.W., Ho S., Holmes S.,
 RA Hunt S.E., Jones M.C., Kershaw J., Kimberley A.M., King A.,
 RA Laird G.K., Langford C.F., Leverisha M.B., Lloyd C., Lloyd D.M.,
 RA McLaren J.D., Mashreghi-Mohammadi M., Matthews L.H., Mccann O.T.,
 RA McElay J., McLaren S., McMurray A.A., Milne S.A., Mortimore B.J.,
 RA Odell C.N., Pavitt R., Pearce A.V., Pearson D., Phillimore B.J.C.T.,
 RA Phillips S.H., Plumb R.W., Ramsay H., Ramsey Y., Rogers L., Ross M.T.,
 RA Scott C.E., Sehra H.K., Skuce C.D., Smalley S., Smith M.L.,
 RA Soderlund C., Spragon L., Steward C.A., Sulston J.E., Swann R.M.,
 RA Vaudin M., Wall M., Wallis J.M., Whiteley M.N., Willey D.L.,
 RA Williams L., Williams S.A., Williamson H., Wilmer T.E., Wilming L.,
 RA Wright C.L., Hubbard T., Bentley D.R., Beck S., Rogers J., Shimizu N.,
 RA Minoshima S., Kawasaki K., Sasaki T., Asakawa S., Kudoh J.,
 RA Shintani A., Shibuya K., Yoshizaki Y., Aoki N., Mitsuyma S.,
 RA Roe B.A., Chen F., Chu L., Crabtree J., Deschamps S., Do A., Do T.,
 RA Dorman A., Fang F., Fu Y., Hu P., Hua A., Kenton S., Lai H., Lao H.I.,
 RA Lewis J., Lewis S., Lin S.-P., Loh P., Malaj E., Nguyen T., Pan H.,

RA Phan S., Qi S., Qian Y., Ray L., Ren Q., Shauli S., Sloan D., Song L.,
 RA Wang Q., Wang Y., Wang Z., White J., Williamson D., Wu H., Yao Z.,
 RA Zhan M., Zhang G., Chisoe S., Murray J., Miller N., Minx P.,
 RA Fulton R., Johnson D., Bemis G., Bentley D., Bradshaw H., Bourne S.,
 RA Cordes M., Du Z., Fulton L., Goela D., Graves T., Hawkins J.,
 RA Hinds K., Kemp K., Latreille P., Layman D., Ozerisky P., Rohlfing T.,
 RA Schert P., Walker C., Wamsley A., Wohlmann P., Pepin K., Nelson J.,
 RA Korf I., Bedell J.A., Hillier L., Maris E., Waterston R., Wilson R.,
 RA Emanuel B.S., Shaikh T., Kurahashi H., Saita S., Budarf M.L.,
 RA Mcdermid H.E., Johnson A., Wong A.C.C., Morrow B.E., Edelmann L.,
 RA Kim U.J., Shizuya H., Simon M.I., Dunamski J.P., Peyrard M., Kedra D.,
 RA Seroussi E., Fransson I., Tapia I., Bruder C.E., O'Brien K.P.,
 RA Wilkinson P., Bodenreich A., Hartman K., Hu X., Khan A.S., Lane L.,
 RA Tilahun Y., Wright H.,
 RT "The DNA sequence of human chromosome 22.",
 RL Nature 402:489-495(1999).
 RN [3]
 RP SEQUENCE OF 624-3014 FROM N.A. (ISOFORM 2).
 RC TISSUE=Kidney;
 RA Strausberg R.;
 RL Submitted (NOV-2000) to the EMBL/Genbank/DBJ databases.
 CC -!- FUNCTION: Receptor that may have an important role in cell/cell
 CC signaling during nervous system formation.
 CC -!- SUBCELLULAR LOCATION: Integral membrane protein.
 CC -!- ALTERNATIVE PRODUCTS: 2 isoforms; 1 (shown here) and 2; may be
 CC produced by alternative splicing.
 CC -!- SIMILARITY: BELONGS TO FAMILY 2 OF G-PROTEIN COUPLED RECEPTORS.
 CC -!- SIMILARITY: CONTAINS 9 CADERLIN DOMAINS.
 CC -!- SIMILARITY: CONTAINS 8 EGF-LIKE DOMAINS.
 CC -!- SIMILARITY: CONTAINS 2 LAMININ G-LIKE DOMAINS.
 CC -!- SIMILARITY: CONTAINS 1 LAMININ EGF-LIKE DOMAIN.
 CC -!- SIMILARITY: CONTAINS 1 GPS DOMAIN.
 CC -----
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 CC -----
 CC EMBL, AF231024; AAF61930.1; -
 CC EMBL, AL021392; CAB50707.1; -
 CC EMBL, AL031597; CAB5020.1; ALU_INIT.
 CC EMBL, AL031588; CAB38413.1; -
 CC EMBL, BC000059; AAH00059.1; -
 CC Genew; HGNC:1850; CELSRL.
 CC MIM; 604523; -
 CC HSSP; P00749; 10RK.
 DR InterPro; IPR000152; Asx_hydroxyl.
 DR InterPro; IPR002126; Caderlin.
 DR InterPro; IPR000561; EGF-like.
 DR InterPro; IPR000832; GPCR_secretin.
 DR InterPro; IPR001879; hormu_receptor.
 DR InterPro; IPR002049; laminin_EGF.
 DR InterPro; IPR001791; laminin_G.
 DR InterPro; IPR000203; PKD_cys-rich.
 DR Pfam; PF00002; 7tm_2; 1.
 DR Pfam; PF00028; caderlin; 8.
 DR Pfam; PF00008; EGF; 6.
 DR Pfam; PF01825; GPS; 1.
 DR Pfam; PF02793; HRM; 1.
 DR Pfam; PF00054; laminin_G; 1.
 DR PRINTS; PR00205; CADERLIN.
 DR PRINTS; PR00011; EGF_LAMININ.
 DR PRINTS; PR00249; GPCRSECRETIN.
 DR SMART; SM00112; CA; 9.
 DR SMART; SM00180; EGF_Lam; 1.
 DR SMART; SM00001; EGF_Like; 6.
 DR SMART; SM00303; GPS; 1.
 DR SMART; SM00008; Hormn; 1.
 DR SMART; SM00282; Lamg; 2.
 DR PROSITE; PS00010; ASX_HYDROXYL; 2.

DR PROSITE; PS00232; CADHERIN_1; 7.
 DR PROSITE; PS00268; CADHERIN_2; 9.
 DR PROSITE; PS00022; EGF_1; 6.
 DR PROSITE; PS01186; EGF_2; 2.
 DR PROSITE; PS00221; GFS-1.
 DR PROSITE; PS00649; G-PROTEIN_RECP_F2_1; FALSE_NEG.
 DR PROSITE; PS00650; G-PROTEIN_RECP_F2_2; FALSE_NEG.
 DR PROSITE; PS00227; G-PROTEIN_RECP_F2_3; 1.
 DR PROSITE; PS00261; G-PROTEIN_RECP_F2_4; 1.
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 DR PROSITE; PS00025; LAM_G_DOMAIN; 2.
 KW G-protein coupled receptor; Transmembrane; Glycoprotein;
 KW EGF-like domain; Calcium-binding; Laminin EGF-like domain; Repeat;
 KW Developmental protein; Hydroxylation; Signal; Alternative splicing.
 FT SIGMUL 1 20
 FT CHAIN 21 3014
 FT DOMAIN 22 2469
 FT TRANSMEM 2470 2490
 FT DOMAIN 2491 2501
 FT TRANSMEM 2502 2522
 FT DOMAIN 2523 2527
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 FT DISULFID 1911 1922
 FT DISULFID 1916 1934
 FT DISULFID 1936 1945
 FT DISULFID 1945 1963

FT DISULFID 1953 1966 BY SIMILARITY.
 FT DISULFID 1968 1978 BY SIMILARITY.
 FT DISULFID 1985 2000 BY SIMILARITY.
 FT DISULFID 1987 2003 BY SIMILARITY.
 FT DISULFID 2005 2015 BY SIMILARITY.
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 Best local Similarity 24.3%; Pred. No. 1,4e-36;
 Matches 236; Conservative 141; Mismatches 338; Indels 256; Gaps 35;
 QY 17 VRAMDVLGLDVLQRLRLTGGKDSAA---RSLNKAMVEIVNNLQPOLNARDLTSD 73
 DB 2153 VRYAYOLLG---HYLQHSWQOQFDLAATODADHEDVHGSALLAPYRAAEQIOESE 2210
 QY 74 OLRAATGLTIVE-----ESAVLNDLTKTIVENTDNILEVARLS 117
 DB 2211 --GTAQLRLRLGYSNVARNRRTYLRFFVITYTANMILAVIF---DKENFTGARVP 2264
 QY 118 TEGNLEDLPENMGHSTIOLSAN-----TLKONGRN----- 150
 DB 2265 RPDTHIE-EPREL--ESSVSPADFPPEPEKEGPLLRPAGRRTYQPTRPGETEREA 2321
 QY 151 -----GEIRAPV-LYNNIGPVY-----STENASMKTEALSTNHSYVNSPY 193
 DB 2322 PISRRRRHPDDAQOFAVALVITYRLGQLPERYDPRSLRL-----PHRPIINTPM 2374
 QY 194 ITAINKPEFNKYVLDPV---VETVKHIKSENFNPNCSEFYSKRT-MTGYSWTOGC 249
 DB 2375 VSTLV---YEGAPLPPELPVLPVEFALLEVEREKPVCFVFNHSLAVGTGCKWARGC 2431
 QY 250 RLITNKTHTTSCNHLTNFAVLMANHEVKSDAVDHLLDVTWVGILLSLVCLICIF 309
 DB 2432 ELSRNTHVACQCSHTASPAVLM---DISRRENGEVLPIKITYAAVSLAALLVAEV 2488
 QY 310 TPFEEFRLQDRMTIHKNCISLFEVALLFDLGINRPDQIACAVPRAALLHFFLAFTW 369
 DB 2489 LLSLVRLRLKSNLHSIRKHLVALFLSOLVFLVGINOTENPFLTVAAILHYTMSTFAW 2348
 QY 370 MLEGVOLYLMLVEFESEHSRRKRYFLVGYGMPALIVAAVAADVRSYGTDRVCWLRD 429
 DB 2549 TLVESLHVHYMLEVRNIDGPMRFYVVGWGIPIATVIGLAVLDQGYGNPFCMLSLQ 2608
 QY 430 TYPTWSEFGPATLLIMLVNFIIGIALYKMFHRAILKPESGC-----LDNIKSMVIG 481
 DB 2609 DFLIWSFAPGIGAVIITNV-----TSVLAKVSCORKNHHYVKKGIVSLIRT 2656
 QY 482 AIALLCILGLTMAFGMLYNVESTIVIMAYLFTINSLOGMFIFFHCYLOKKVKEKCKL 541
 DB 2657 AFLLLLSATYTWLLGLAVNRDALSFHYLFAIFSGLOGPVLVLCVLANQEVRRHLKGYL 2716
 QY 542 ---RTHCCSGKSTES-----SIGSGKTSGS-----RTPGRYSTGSQSRIRRMNDTVRKQ 588
 DB 2717 GGRKLHEDSATIRATRLTSLNLCNTTFGDPGPMRLTDLGEASTASLDSTYR--DEGIQIL 2774
 QY 589 SESSFITGDNSSASLNREGILNNAARDYSVDTPLPNGNHGSSYASISGEFYSNCOVIID 648
 DB 2775 GVSS-----GL-----VRSGHGEDA-----SLMP 2794
 QY 649 RGY-----NNHETLEKKIKELTSLNTPSYLNNHSSSEQNRMLKLVNNGSGEDDA 704
 DB 2795 RSCKDPGHDSDSDSELSDEOSS---SYASSHSSSEDD-----GVGAEEK- 2838
 QY 705 IVLDDATSFHHEESLG-----LELHESDAPLPPRY-----YSTENHOPH 746
 DB 2839 --WDPARGAVHSTPKGDVAHVHPAGPPOSLSSESDEPGRKLKVEKYSVELHREE 2896
 QY 747 HYTRRRIPQDHSFPPLTNEHTEDLQSPHRDSLTYSTPLTLAGVATESVTTSTQTEPP 806
 DB 2897 QGSHR-----GEYPPQESGGAARLASSQPP-----DQRGILKNKVTYTP 2937
 QY 807 P-----AKCGAED-----VYKSPNGLSRNHVHQLRT 835
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QY	836	YYOLRGSSDG	846
DB	2998	NVRTGSAQADG	3008
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ID	CLIR2_RAT	STANDARD:	PRT: 2144 AA.
AC	O90YP2;		
DT	15-JUN-2002 (Rel. 41, Created)		
DT	15-JUN-2002 (Rel. 41, Last sequence update)		
DT	15-JUN-2002 (Rel. 41, Last annotation update)		
DE	Cadherin EGF LAG seven-pass G-type receptor 2 (multiple epidermal growth factor-like domains 3) (Fragment).		
GN	CERS2 OR MEGF3.		
OS	Rattus norvegicus (Rat).		
OC	Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi; Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Rattus.		
OX	NCBI_TaxID=10116;		
RN	[1]		
RP	SEQUENCE FROM N.A.		
RC	SFRAIN-Sprague-Dawley; TISSUE=Brain;		
RA	MEDLINE=98360089; PubMed=9693030.		
RT	Nakayama M., Nakajima D., Nagase T., Nomura N., Seki N., Ohara O.;		
RT	"Identification of high-molecular-weight proteins with multiple EGF-like motifs by motif-trap screening.";		
RL	Genomics 51:27-34(1998).		
CC	-1- FUNCTION: Receptor that may have an important role in cell/cell signaling during nervous system formation.		
CC	-1- SUBCELLULAR LOCATION: Integral membrane protein.		
CC	-1- TISSUE SPECIFICITY: Expressed in the brain. High expression in cerebellum and olfactory bulb. Weaker expression in cerebral cortex, hippocampus and brain stem.		
CC	-1- SIMILARITY: BELONGS TO FAMILY 2 OF G-PROTEIN COUPLED RECEPTORS.		
CC	-1- SIMILARITY: CONTAINS 4 CADHERIN DOMAINS.		
CC	-1- SIMILARITY: CONTAINS 8 EGF-LIKE DOMAINS.		
CC	-1- SIMILARITY: CONTAINS 2 LAMININ G-LIKE DOMAINS.		
CC	-1- SIMILARITY: CONTAINS 1 LAMININ EGF-LIKE DOMAIN.		
CC	-1- SIMILARITY: CONTAINS 1 GPS DOMAIN.		
CC	-----		
CC	CC This SWISS-PROT entry is copyright. It is produced through a collaboration between the Swiss Institute of Bioinformatics and the EMBL outstation - the European Bioinformatics Institute. There are no restrictions on its use by non-profit institutions as long as its content is in no way modified and this statement is not removed. Usage by and for commercial entities requires a license agreement (see http://www.isb.ch/announce/ or send an email to license@isb-sib.ch).		
CC	-----		
DR	EMBL; AB011529; BAA8687.1; -		
DR	HSSP; P00740; IEDM.		
DR	InterPro: IPR000152; Asx_hydroxyl.		
DR	InterPro: IPR002126; Cadherin.		
DR	InterPro: IPR000561; EGF-like.		
DR	InterPro: IPR000742; EGF 2.		
DR	InterPro: IPR001881; EGF Ca.		
DR	InterPro: IPR001438; EGF-IT.		
DR	InterPro: IPR000832; GPCR_secretin.		
DR	InterPro: IPR001879; hormn_receptor.		
DR	InterPro: IPR002049; Laminin_EGF.		
DR	InterPro: IPR001791; Laminin G.		
DR	InterPro: IPR000203; PKD_cys-rich.		
DR	Pfam; PF00002; 7tm_2; 1.		
DR	Pfam; PF00028; cadherin; 3.		
DR	Pfam; PF00008; EGF; 6.		
DR	Pfam; PF01825; GPS; 1.		
DR	Pfam; PF02793; HRM; 1.		
DR	Pfam; PF00054; laminin_G; 1.		
DR	PRINTS; PR00205; CADHERIN.		
DR	PRINTS; PR00010; EGFBLDIN.		
DR	PRINTS; PR00011; EGF_LAMININ.		
DR	PRINTS; PR00249; GPCRSECRETIN.		
DR	SMART; SM00112; CA; 3.		

[illegible]

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FT DISULFID 1149 1161 BY SIMILARITY.
FT DISULFID 1151 1168 BY SIMILARITY.
FT DISULFID 1170 1179 BY SIMILARITY.
FT MOD_RES 816 816 HYDROXYLATION (POTENTIAL).
FT MOD_RES 1035 1035 HYDROXYLATION (POTENTIAL).
FT CARBOHYD 261 261 N-LINKED (GLCNAC. . .) (POTENTIAL).
FT CARBOHYD 301 301 N-LINKED (GLCNAC. . .) (POTENTIAL).
FT CARBOHYD 407 407 N-LINKED (GLCNAC. . .) (POTENTIAL).
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SQ SEQUENCE 2144 AA; 233480 MW; 66A898C1BA655E6A CRC64;

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Query Match 14.0%; Score 637.5; DB 1; Length 2144;
Best Local Similarity 26.9%; Pred. No. 3,1e-33;
Matches 180; Conservative 107; Mismatches 258; Indels 123; Gaps 19;

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QY 46 LNKAMETVNN-----LLOPOLANMWDLTTSQDLRAATMLHTVEESAFLADNLLKT- 99
DB 1336 VGSALLDAAKRHWELIQTEGGTAW-----LQHYEAYASALQNMHRHY 1381
QY 100 -----DIVRENTDNINKLEVALNSTEGNEDLKF----- 128
DB 1382 LSPFTYI--TPNIVISVRLD-KGNPAGTKLPREYALRGERPPDETTVILPESVREM 1437
QY 129 -----ENMGHSTQLSANTLKONGR-----NGEIRVAFVLNNLCPLYSTENASMKLTGEA 180
DB 1438 PMWVRSAGPEEADETEELARQRHRELPSGEAVASVYIIHTLGLLPHNYDPK---RS 1494
QY 181 LSTNHSYIVNPIYTAINKFEFSNKYVLADPVVYFKHIOSEENFNPNCSFMSYSKRTM 240
DB 1495 LRPVKKRPIVNTPVYVSIHVHDEELLPRALDKPVYQFRLLTEBRTKPICVFNHSHIVS 1554
QY 241 -TGVWSOGORLTLTKNTHTCSCNHLTNFAVLMAHYEVKSDAVNHLDDLVTWVILL 299
DB 1555 GTGWSMGRGEEVFNESHVSCCNHMTSFAVLN---DVSRRREGETLPLKTLTYVALGV 1611
QY 300 SLVCLLICITFCFFRGLQSDRMTIHKNCISLFEVALLFLIGINTPTDPIACAVFALL 359
DB 1612 TLAAIMTFELFLRLRLBRNONGIRNLNALGLQADYVELLGINQADLPFACIVAILL 1671
QY 360 HFFFLAAFTWMLLEGVOLYIMLVEVESEHSRRKRYFLVGYGMPALIVAVSAVDYRSYG 419
DB 1672 HFLYLCFFSWALLEALYLBALTEVRDVNASPMRFYMLGMVPAFTIGLAVGDPEGYG 1731
QY 420 TDVVCWRLDTYFLWISIGPATLIMLVFLGIALYKMHHTAILKPEGCIDNIR--- 476
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QY 477 -----SWVIGAILLCLLGTMAFGLMYINESTVIMAYLFTIENSLOGMFIFFHYCLOK 531
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QY 532 KVRKEGKCLRTIHCCSGKSTESSI--GSGKTSGRPRPGRYSTGSQSHIRMMMDTVARK-- 587
DB 1840 EVR-----KALKFACSRKRPSPDPAITKSTLTSSVNCPSPYADG---RLYQPGDSAGSLH 1892
QY 588 -----QSESEFTGDINSSASLN-----REGLLNNAK-----TTSVMDTLPN 625
DB 1893 SASRSGSGQSYLIPFLURESTLNPQGVPPGLADPSGLFMEGQAQOHDPTDSDSLSL 1952
QY 626 GNHGNSTYS 633
DB 1953 DDGSGSYA 1960

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RESULT 7
CLR2_HUMAN
ID CLR2_HUMAN STANDARD; PRT; 2923 AA.
AC 09HC04; 092566;
DT 15-JUN-2002 (Rel. 41, Created)
DT 15-JUN-2002 (Rel. 41, Last sequence update)
DT 15-JUN-2002 (Rel. 41, Last annotation update)
DE Cadherin EGF LAG seven-pass G-type receptor 2 precursor (Epidermal
DE growth factor-like 2) (Multiple epidermal growth factor-like domains
DE 3) (Flamingo 2).
GN CELSR2 OR CHERF10 OR EGF2 OR MECF3 OR KIA0279.
OS Homo sapiens (human).
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC Mammalia; Eutheria; Primates; Catarrhini; Homiidae; Homo.
OX NCBI_TaxId=9606;
RN [1]
RP SEQUENCE FROM N.A.
RX MEDLINE=20363102; PubMed=10907856;
RA Vincent J.B., Skaug J., Scherer S.M.;
RT "The human homologue of flamingo, EGF2, encodes a brain-expressed
RT large cadherin-like protein with epidermal growth factor-like domains,
RT and maps to chromosome 1p13.3-p21.1."
RL DNA Res. 7:233-235(2000).
RN [2]
RP SEQUENCE OF 516-2923 FROM N.A.
RC TISSUE=Brain;
RX MEDLINE=97191544; PubMed=9039502;
RA Nagase T., Seki N., Ishikawa K.-I., Ohira M., Kawarabayashi Y.,
RA Ohara O., Tanaka A., Kotani H., Miyajima N., Nomura N.;
RT "Prediction of the coding sequences of unidentified human genes. VI.
RT The coding sequences of 80 new genes (KIA0201-KIA0280) deduced by
RT analysis of cDNA clones from cell line KG-1 and brain."
RL DNA Res. 3:321-329(1996).
CC -1- FUNCTION: Receptor that may have an important role in cell/cell
CC signalling during nervous system formation.
CC -1- SUBCELLULAR LOCATION: Integral membrane protein.
CC -1- TISSUE SPECIFICITY: Highest expression in brain and testis.
CC -1- SIMILARITY: BELONGS TO FAMILY 2 OF G-PROTEIN COUPLED RECEPTORS.
CC -1- SIMILARITY: CONTAINS 9 CADHERIN DOMAINS.
CC -1- SIMILARITY: CONTAINS 8 EGF-LIKE DOMAINS.
CC -1- SIMILARITY: CONTAINS 2 LAMININ G-LIKE DOMAINS.
CC -1- SIMILARITY: CONTAINS 1 GPS DOMAIN.
CC
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CC
EMBL: AF234887; AMG00080.1; -.
DR EMBL: D87469; BAI3407.1; -.
DR HSSP: P15116; INCU.
DR GeneW: HGNC:3231; CELSR2.
DR MIM: 604265; -.
DR InterPro: IPR000152; Asx_hydroxyl.
DR InterPro: IPR002126; Cadherin.
DR InterPro: IPR000561; EGF-like.
DR InterPro: IPR000742; EGF-2.
DR InterPro: IPR001881; EGF_Ca.
DR InterPro: IPR000832; GPCR_secretin.
DR InterPro: IPR001879; hormn_receptor.
DR InterPro: IPR002049; laminin_Egf.
DR InterPro: IPR001791; laminin_G.
DR InterPro: IPR000203; PKD_cys-rich.
DR Pfam: PF00002; 7tm_2; 1.
DR Pfam: PF00008; cadherin; 8.
DR Pfam: PF00008; EGF; 6.
DR Pfam: PF01825; GPS; 1.
DR Pfam: PF02793; HRV; 1.
DR Pfam: PF00054; laminin_G; 1.

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Db 2555 KRGVSLQPSFAVLLLSAIFLLVSDTLFFHLFATCICIGPFIFLSYVLSK 2614
QY 532 KVRREYKCLRTGCCSKSTESI--GSGKTSGRTPGRYSTGOSPIRRMMNTVKK-- 587
Db 2615 EVR---KALKACSRKPSDPALTTKSTLTSSINCPSPYADG---RLYQYGDYSGASLH 2667
QY 588 -----QSESSFTTGIDINSSASLN 605
Db 2668 STSRGSKGPSYIPFLRESALN 2691

RESULT 8
CLR2_MOUSE
ID CLR2_MOUSE STANDARD: PRT; 2920 AA.
AC G9ROM0: G92R4; G99K26;
DT 15-JUN-2002 (Rel. 41, Created)
DT 15-JUN-2002 (Rel. 41, Last sequence update)
DE 15-JUN-2002 (Rel. 41, Last annotation update)
DE Cadherin EGF LAG seven-pass G-type receptor 2 precursor (Flamingo 1)
DE (mfam11).
GN CELSR2.
OS Mus musculus (Mouse).
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Mus.
OX NCBI_TaxID=10090;
RN [1]
RP MEDLINE=99418630; PubMed=10490098;
RX Usui T., Shima Y., Shimada Y., Hirano S., Burgess R.W., Schwarz T.L.,
RA Takeichi M., Uemura T.;
RT "Flamingo, a seven-pass transmembrane cadherin, regulates planar cell
RT polarity under the control of frizzled.";
RL Cell 98:585-595(1999).
RN [2]
RP SEQUENCE OF 1913-2796 FROM N.A., AND TISSUE SPECIFICITY.
RX PubMed=10790539;
RA Formstone C.J., Barclay J., Rees M., Little P.F.R.;
RT "Chromosomal localization of Celstr2 and Celstr3 in the mouse: Celstr3 is
RT a candidate for the floppy (fip) lethal mutant on chromosome 9.";
RL Mamm. Genome 11:392-394(2000).
RN [3]
RP SEQUENCE OF 2014-2920 FROM N.A.
RX TISSUE-Breast tumor;
RA Strausberg R.;
RL Submitted (MAR-2001) to the EMBL/GenBank/DBJ databases.
RN [4]
RP DEVELOPMENTAL STAGE.
RX PubMed=11850187;
RA Tissir F., De-Backer O., Goffinet A.M., Lambert de Rouvroit C.A.;
RT "Developmental expression profiles of Celstr (Flamingo) genes in the
RT mouse.";
RL Mech. Dev. 112:157-160(2002).
RN [5]
RP FUNCTION: Receptor that may have an important role in cell/cell
RP signaling during nervous system formation.
RN [6]
RP SUBCELLULAR LOCATION: Integral membrane protein.
RN [7]
RP DEVELOPMENTAL STAGE: Predominantly expressed in the developing
RP CNS, the emerging dorsal root ganglia and cranial ganglia. In the
RP CNS, expression is uniform along the rostrocaudal axis. During
RP gastrulation, it is expressed within the anterior neural ectoderm.
RP At E10, expression is strong in the ventricular zones (VZ) in all
RP sectors of the brain, and lower in the marginal zones (MZ). It is
RP strong in VZ, lower in MZ, except in telecephalic MZ where it is
RP predominant. The intensity is higher in all VZ, and lower in
RP differentiating fields than in VZ, except in the cerebral
RP hemispheres, and to a lesser extent in the tectum and cerebellum.
RP A weak expression is also observed in the fetal lungs, kidney and
RP epithelia. In the newborn and postnatal stages, expression remains
RP restricted to the VZ as well as in migrating and postmigratory
RP cells throughout the brain.
RN [8]
RP TISSUE SPECIFICITY: Expressed in the CNS and in the eye.
RN [9]
RP SIMILARITY: BELONGS TO FAMILY 2 OF G-PROTEIN COUPLED RECEPTORS.

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CC -1- SIMILARITY: CONTAINS 9 CADHERIN DOMAINS.
CC -1- SIMILARITY: CONTAINS 8 EGF-LIKE DOMAINS.
CC -1- SIMILARITY: CONTAINS 2 LAMININ G-LIKE DOMAINS.
CC -1- SIMILARITY: CONTAINS 1 LAMININ EGF-LIKE DOMAIN.
CC -1- SIMILARITY: CONTAINS 1 GPS DOMAIN.
CC -----
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CC -----
DR EMBL: AB028499; BAA84070.1; -.
DR EMBL: AF031573; AAC68837.1; -.
DR EMBL: BC005499; AAH05499.1; -.
DR HSP: P00740; 1EDM.
DR MGD: MGI:1858235; Celstr2.
DR InterPro: IPR000152; Asx_hydroxyl.
DR InterPro: IPR002126; Cadherin.
DR InterPro: IPR000561; EGF-like.
DR InterPro: IPR000742; EGF_2.
DR InterPro: IPR000832; GPCR_secretin.
DR InterPro: IPR001879; hormn_receptor.
DR InterPro: IPR002049; Laminin_EGF.
DR InterPro: IPR001791; Laminin_G.
DR InterPro: IPR002033; PKC_cys-rich.
DR Pfam: PR00002; 7tm_2; 1.
DR Pfam: PF00028; cadherin; 9.
DR Pfam: PF00008; EGF; 5.
DR Pfam: PF01825; GPS; 1.
DR Pfam: PF02793; HRM; 1.
DR Pfam: PF00054; laminin_G; 2.
DR PRINTS: PR00205; CADHERIN.
DR PRINTS: PR00011; EGF_LAMININ.
DR PRINTS: PR00249; GPCRSECRETIN.
DR SMART: SM00112; CA; 9.
DR SMART: SM00180; EGF_Lam; 1.
DR SMART: SM00001; EGF_Like; 6.
DR SMART: SM00303; GPS; 1.
DR SMART: SM00008; Hormr; 1.
DR SMART: SM00282; Lang; 2.
DR PROSITE: PS00010; ASX_HYDROXYL; 1.
DR PROSITE: PS00232; CADHERIN_1; 6.
DR PROSITE: PS0268; CADHERIN_2; 9.
DR PROSITE: PS00022; EGF_1; 6.
DR PROSITE: PS01186; EGF_2; 2.
DR PROSITE: PS00649; G-PROTEIN_RECP_F2_1; FALSE_NEG.
DR PROSITE: PS00650; G-PROTEIN_RECP_F2_2; FALSE_NEG.
DR PROSITE: PS50227; G-PROTEIN_RECP_F2_3; 1.
DR PROSITE: PS50261; G-PROTEIN_RECP_F2_4; 1.
DR PROSITE: PS01248; LAMININ_TYPE_EGF; 1.
DR PROSITE: PS50221; GPS; 1.
DR PROSITE: PS50025; LAM_G_DOMAIN; 2.
KW G-protein coupled receptor; Transmembrane; glycoprotein;
KW EGF-like domain; Calcium-binding; Laminin EGF-like domain; Repeat;
KW Developmental protein; Hydroxylation; Signal.
FT SIGNAL 1 31
FT CHAIN 32 2920
FT DOMAIN 32 2381
FT TRANSSEM 2382 2402
FT TRANSSEM 2403 2414
FT TRANSSEM 2415 2434
FT TRANSSEM 2435 2439
FT TRANSSEM 2440 2460
FT TRANSSEM 2461 2481
FT TRANSSEM 2482 2502
FT TRANSSEM 2503 2519
FT TRANSSEM 2520 2540
FT TRANSSEM 2541 2564
FT TRANSSEM 2565 2585

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Query Match	Best Local Similarity	Score	DB 1:	Length
Matches 176;	Conservative 110;	Mismatches 259;	Indels 123;	Gaps 19;

46 LNKAVEYVNN-----LLOPOLNANRDLTTSDQLRAATMLHTVEESAFVLADNLKLT- 99
 Db 2112 VGSALLDANKRRMELIOQEGTAW-----LLOHYAYASALAQNRRHY 2157
 QY 100 ----DIVRENTDNKLEVARLSTEGNLEDKFP----- 128
 Db 2158 LSPFTIV---TPNIVISVRLD-KGNPAGTKLPREYALNGERPDPVETVILPESEVREM 2213
 QY 129 ----EMMGHSTIQLSANILKONGR-----NGELRVAFLVLYNNIGPLSTFNASKLGTET 180
 Db 2214 PSMVRSGPREAOETBELARRORRHPELSOGEVAVASVITYHTLAGLLPHNYDPDK---RS 2270
 QY 181 LSTNHSVIYNSPVITAIKNEFSNKVYLADPVYFVKHIOSEENPNPSCFMSYKRTM 240
 Db 2271 LRPKRPVINTPRAVSIYHDEDELIRALDKPVTQVFRLETERKPKICVFNNHSILVS 2330
 QY 241 -TGWSTOGRLLTTRTKHTTCSNHLTNFAVLMHAHEVYKHSDAVDLLDVTWVGILL 299
 Db 2331 GTGGMWARGCEVYERFRESHVSCCNHMTSPAVLM---DMSRRENGEILPLKTLTYVALGV 2387
 QY 300 SLVCLLICITFTCFEFGLOSDRNTIKNICISLFAVELLFLGINRTDPIACAVPAALL 359
 Db 2388 TLAAMLLTFELTTLRALRNSNGIRNLTAAIGLQVFLGINQADLPFACTVIAILL 2447
 QY 360 HFFFLAFTWFMLEGVQLYIMLVEFESEHSRRKRYLVGCGPALITAVNSAADVRSYG 419
 Db 2448 HFLYLCFTSPALLALHLIRALTEVRDVANSPRRFYMLGWPALITGLAVLDEGIG 2507
 QY 420 TDRWMLRDLFTYFWSFGPATLLIMLVFLGIALYKMHHTALIKPESGIDNIK--- 476
 Db 2508 NPFCWLSYVDLIMSFAGVAFVMSVFE---LY-----ILSARSCAAQOGFE 2555
 QY 477 -----SMVIGAILDLGLITAFGLMYTNESTVIMAYLFTTINSQGMFIFFHCYLOK 531
 Db 2556 KKGVPVGLRSSFTVLLLSATWLLALLSVNSDPLLFHYMAQNCVQGPFTISYVLSK 2615
 QY 532 KVRKEXGKCLRTCCSGKSTRESSIGS--GKTSGRTPGRSTSGSQRIRMMNDVYRK-- 587
 Db 2616 EVR-----KALKFACSKRPPSPDPAITTKYTLTSSYNCPSPADG---RLIOPYDSAGSLH 2668
 QY 588 -----QSESSFTTGDIINSSASLN-----REGLLNNAR-----DTSYMDTLPLN 625
 Db 2669 SASRSGKSQSYIPFLIRESTLNPQVPGPLDPSGLFLEGQAQHDPTDSDLSLE 2728
 QY 626 GNGHNSYS 633
 Db 2729 DDQSGSYA 2736

RESULT 9
 ID BAI3_HUMAN STANDARD; PRT; 1522 AA.
 AC 060242; 060297;
 DT 16-OCT-2001 (Rel. 40, Created)
 DT 16-OCT-2001 (Rel. 40, Last sequence update)
 DT 15-JUN-2002 (Rel. 41, Last annotation update)
 DE Brain-specific angiogenesis inhibitor 3 precursor.
 GN BAI3 OR KIAA0550.
 OS Homo sapiens (Human).
 OC Eukaryota; Metazoa; Chordata; Vertebrata; Euteleostomi;
 OC Mammalia; Euteria; Primates; Catarrhini; Hominoidea; Homo.
 OX NCBI_Taxid=9606;
 RP SEQUENCE FROM N.A. (LONG ISOFORM).
 RC TISSUE=Petal Brain;
 RX MEDLINE=98194217; PubMed=9533023;
 RA Shiratsuchi T., Nishimori H., Ichise H., Nakamura Y., Tokino T.;
 RT "Cloning and characterization of BAI2 and BAI3, novel genes homologous
 to Brain-specific angiogenesis inhibitor 1 (BAI1).";
 RL Cytogenet. Cell Genet. 79:103-108(1997).
 RN [2]
 RC SEQUENCE FROM N.A. (SHORT ISOFORM).
 RC TISSUE=Brain;

RX MEDLINE-98290545; PubMed-9628581;
 RA Nagase T., Ishikawa K.-I., Miyajima N., Tanaka A., Kotani H.,
 RA Nomura N., Oshara O.;
 RT "Prediction of the coding sequences of unidentified human genes. IX.
 RT The complete sequences of 100 new cDNA clones from brain which can
 RT code for large proteins in vitro.";
 RL DNA Res. 5:31-39(1998).
 CC -1- FUNCTION: MIGHT BE INVOLVED IN ANGIOGENESIS INHIBITION AND
 CC SUPPRESSION OF GLOBLASTOMA.
 CC -1- SUBCELLULAR LOCATION: Integral membrane protein.
 CC -1- ALTERNATIVE PRODUCTS: 2 ISOFORMS: A LONG FORM (SHOWN HERE) AND A
 CC SHORT FORM. MAY BE PRODUCED BY ALTERNATIVE SPLICING.
 CC -1- TISSUE SPECIFICITY: STRONGLY EXPRESSED IN BRAIN. ALSO DETECTED IN
 CC HEART. REDUCED EXPRESSION IS OBSERVED IN SOME GLOBLASTOMA CELL
 CC LINES.
 CC -1- SIMILARITY: BELONGS TO FAMILY 2 OF G-PROTEIN COUPLED RECEPTORS.
 CC -1- SIMILARITY: CONTAINS 1 CUB DOMAIN.
 CC -1- SIMILARITY: CONTAINS 4 TSP TYPE-1 DOMAINS.
 CC -1- SIMILARITY: CONTAINS 1 GPS DOMAIN.
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 DR EMBL: AB005299; BAA25363.1; -;
 DR EMBL: AB011122; BAA25476.1; -;
 DR Genev: HGNC:945; BA13.
 DR MIM: 602684; -;
 DR InterPro: IPR000859; CUB_domain.
 DR InterPro: IPR000832; GPCR_secretin.
 DR InterPro: IPR000203; PKD_cys_rich.
 DR InterPro: IPR000884; TSP1.
 DR InterPro: IPR001879; horml_receptor.
 DR Pfam: PF00002; 7tm_2; 1.
 DR Pfam: PF00090; tsp_1; 4.
 DR Pfam: PF01825; GPS; 1.
 DR Pfam: PF02793; HRM; 1.
 DR SMART: SM00303; GPS; 1.
 DR SMART: SM00008; HOXMR; 1.
 DR SMART: SM00209; TSP1; 4.
 DR PROSITE: PS01180; CUB; 1.
 DR PROSITE: PS0221; GPS; 1.
 DR PROSITE: PS00649; G_PROTEIN_RECP_F2_1; FALSE_NEG.
 DR PROSITE: PS00650; G_PROTEIN_RECP_F2_2; FALSE_NEG.
 DR PROSITE: PS0227; G_PROTEIN_RECP_F2_3; 1.
 DR PROSITE: PS0261; G_PROTEIN_RECP_F2_4; 1.
 DR PROSITE: PS50092; TSP1; 4.
 DR G-protein coupled receptor; Transmembrane; Glycoprotein; signal;
 KW Repeat; Alternative splicing.
 FT SIGNAL 1 24
 FT CHAIN 25 1522
 FT DOMAIN 25 880
 FT TRANSMEM 881 901
 FT DOMAIN 902 910
 FT TRANSMEM 911 931
 FT DOMAIN 932 939
 FT TRANSMEM 940 960
 FT DOMAIN 961 981
 FT TRANSMEM 982 1002
 FT DOMAIN 1003 1023
 FT TRANSMEM 1024 1044
 FT DOMAIN 1045 1098
 FT TRANSMEM 1099 1119
 FT DOMAIN 1120 1125
 FT TRANSMEM 1126 1146
 FT DOMAIN 1147 1522
 FT TRANSMEM 1523 159
 FT DOMAIN 159 344
 FT TRANSMEM 345 399
 FT DOMAIN 399 399

FT DOMAIN 400 454 TSP TYPE-1 3.
 FT DOMAIN 455 509 TSP TYPE-1 4.
 FT DOMAIN 516 868 GPS.
 FT DOMAIN 942 945 POLY-THR.
 FT DOMAIN 1173 1176 POLY-SER.
 FT CARBOHYD 51 51 N-LINKED (GLCNAC. . .) (POTENTIAL).
 FT CARBOHYD 54 54 N-LINKED (GLCNAC. . .) (POTENTIAL).
 FT CARBOHYD 82 82 N-LINKED (GLCNAC. . .) (POTENTIAL).
 FT CARBOHYD 105 105 N-LINKED (GLCNAC. . .) (POTENTIAL).
 FT CARBOHYD 241 241 N-LINKED (GLCNAC. . .) (POTENTIAL).
 FT CARBOHYD 337 337 N-LINKED (GLCNAC. . .) (POTENTIAL).
 FT CARBOHYD 418 418 N-LINKED (GLCNAC. . .) (POTENTIAL).
 FT CARBOHYD 540 540 N-LINKED (GLCNAC. . .) (POTENTIAL).
 FT CARBOHYD 625 625 N-LINKED (GLCNAC. . .) (POTENTIAL).
 FT CARBOHYD 779 779 N-LINKED (GLCNAC. . .) (POTENTIAL).
 FT CARBOHYD 812 812 N-LINKED (GLCNAC. . .) (POTENTIAL).
 FT CARBOHYD 828 828 N-LINKED (GLCNAC. . .) (POTENTIAL).
 FT CARBOHYD 937 937 N-LINKED (GLCNAC. . .) (POTENTIAL).
 FT CARBOHYD 643 665 MISSING (IN SHORT ISOFORM).
 FT VARSPLIC 990 1007 LPAIVATSVGFRTTGY -> KHIDIPHALKMTLNTH
 FT VARSPLIC 1007 1007 (IN SHORT ISOFORM).
 FT VARSPLIC 1008 1522 MISSING (IN SHORT ISOFORM).
 FT VARSPLIC 1522 AA; 171490 MM; D22D0A5D4BB62502 CRC64;
 SQ SEQUENCE
 Query Match 12.7%; Score 578.5; DB 1; Length 1522;
 Best Local Similarity 22.7%; Pred. No. 1,3e-29;
 Matches 225; Conservative 163; Mismatches 342; Indels 263; Gaps 39;
 QY 5 RNHLNAGDIITYSVRAMDQVLGLDVOLRNLTTPGSKDAS--ARSLNKAMVETVNNLQPQ 61
 DB 608 RKNFYAGDLDLMSVEI-----LRNVDTFRKRSYIPASDGVNPFQIYSLNLDDE 656
 QY 62 ALNARDLTTSDDLRATM-LTHTVESAFVLADNLKTDIVRENTDNIRKLEVARLSTEG 120
 DB 657 NKEKWD---AQQLPSIELMQVIEDFHHVGMGMDFQNSYMTGNNVVASIQKLPAA 713
 QY 121 NLEDKFPENMGHSTQLSANTLKQNGEIRVAE----- 157
 DB 714 VLTDINPFMRGRK-----NVDAWRSSEDPVPIKSTFTPVSSKEIDESSVEYIGA 764
 QY 158 VLYNNLGPYLTENASMKLGTALSTNHSIVNSPVTAANKFSN-----KYLLDPV 212
 DB 765 VLYKNDLILPT-----LRNYVINSKIIVTIRPEPKTDSLELELA--- 808
 QY 213 VETVKKIKOSEENFNPCSEFWSYKRTMT-GYSTGCRLLTNTKTTSCNLTTFEAV 271
 DB 809 -----HL--ANGTLNPRCYVLMDSKTNESLGTMSTGCKTVLDAHTKICDLRSTFAI 861
 QY 272 LMAHVEYKHSDAVHDLDD-----VTTWGIILSLVCL-ICITFCFRGLQSDRNTI 324
 DB 862 L-----AQOPREIIMESGTPSVTLIVSGSLCLALTLLAVVAALMRYIRISERSII 913
 QY 325 HKNLCISLFAVELLFLGINRTDPIACAVEFAALLHFFPLAFAFWMLLEGQVLYIMVEV 384
 DB 914 LINCLEIISNILLIVGOTHTANKSICTTTALHFFLAFSCVLTETAMOSTMAVTK 973
 QY 385 FESEHSRRKTYFLVGYMPALIVASAA-VDRYSYGTDKVCWRLDYTFITSEFGPATLI 443
 DB 974 IRTLILIKR-FLCGWGLPALIVATSVGFTRTKGYGDHICWLSLEGGLYAFVGAAPAAV 1032
 QY 444 IMLNVITGLTALY-----KMFHHTA--LAKESG-CLDNISWYIGAILA---- 485
 DB 1033 VLVNMY-IGILVFNKLVSRDGIIDKKLHRAGOWSEPHSGILLCAKCGVAYSTLATS 1091
 QY 486 -----LCILGLTMAFGWLYINES-VVIMAYLFTFINSLOGMFIFEHCVLO 530
 DB 1092 ASNMASLWSSCVVLPALALWMSAVLAMDKRSILPQLILFAVDSIQGVIYAWHICUL 1151
 QY 531 KKYRKEVKGCLRTCCSGKSTESSIGSGKTSGRTPRGVSTGSOSRIIRMMNDTVRQSE 590
 DB 1152 REVQDAF-RCLRINC-----GPDINADSS 1174
 QY 591 SSFTTG-----DINSSASLNRE-GLLNARDTSVMDTLPLNGN-----HG 629

FT	DISULFID	1370	1381	BY SIMILIARITY.
FT	DISULFID	1375	1412	BY SIMILIARITY.
FT	DISULFID	1414	1423	BY SIMILIARITY.
FT	DISULFID	1430	1441	BY SIMILIARITY.
FT	DISULFID	1435	1450	BY SIMILIARITY.
FT	DISULFID	1452	1461	BY SIMILIARITY.
FT	DISULFID	1470	1481	BY SIMILIARITY.
FT	DISULFID	1475	1491	BY SIMILIARITY.
FT	DISULFID	1493	1504	BY SIMILIARITY.
FT	DISULFID	1717	1728	BY SIMILIARITY.
FT	DISULFID	1722	1737	BY SIMILIARITY.
FT	DISULFID	1739	1748	BY SIMILIARITY.
FT	DISULFID	1941	1952	BY SIMILIARITY.
FT	DISULFID	1946	1961	BY SIMILIARITY.
FT	DISULFID	1963	1972	BY SIMILIARITY.
FT	DISULFID	1976	1987	BY SIMILIARITY.
FT	DISULFID	1981	1999	BY SIMILIARITY.
FT	DISULFID	2001	2010	BY SIMILIARITY.
FT	DISULFID	2010	2028	BY SIMILIARITY.
FT	DISULFID	2018	2031	BY SIMILIARITY.
FT	DISULFID	2033	2043	BY SIMILIARITY.
FT	DISULFID	2050	2065	BY SIMILIARITY.
FT	DISULFID	2052	2068	BY SIMILIARITY.
FT	DISULFID	2070	2080	BY SIMILIARITY.
FT	MOD. RES.	1954	1954	HYDROXYLATION (POTENTIAL).
FT	CARBOHYD	623	623	N-LINKED (GLCNAC. . .) (POTENTIAL).
FT	CARBOHYD	838	838	N-LINKED (GLCNAC. . .) (POTENTIAL).
FT	CARBOHYD	1173	1173	N-LINKED (GLCNAC. . .) (POTENTIAL).
FT	CARBOHYD	1213	1213	N-LINKED (GLCNAC. . .) (POTENTIAL).
FT	CARBOHYD	1308	1308	N-LINKED (GLCNAC. . .) (POTENTIAL).
FT	CARBOHYD	1318	1318	N-LINKED (GLCNAC. . .) (POTENTIAL).
FT	CARBOHYD	1640	1640	N-LINKED (GLCNAC. . .) (POTENTIAL).
FT	CARBOHYD	1704	1704	N-LINKED (GLCNAC. . .) (POTENTIAL).
FT	CARBOHYD	1761	1761	N-LINKED (GLCNAC. . .) (POTENTIAL).
FT	CARBOHYD	2044	2044	N-LINKED (GLCNAC. . .) (POTENTIAL).
FT	CARBOHYD	2173	2173	N-LINKED (GLCNAC. . .) (POTENTIAL).
FT	CARBOHYD	2192	2192	N-LINKED (GLCNAC. . .) (POTENTIAL).
FT	CARBOHYD	2382	2382	N-LINKED (GLCNAC. . .) (POTENTIAL).
FT	CARBOHYD	2472	2472	N-LINKED (GLCNAC. . .) (POTENTIAL).
FT	CARBOHYD	2504	2504	N-LINKED (GLCNAC. . .) (POTENTIAL).
30	SEQUENCE	3313	AA: 359348	MM: B1BLD09517288764
				CRC64;

[illegible]

OY	414	DYRSGYDKNVOMLADYTFIMSPFGATLIMLVNFEGLALCKMHNHAILKPPSGCLD	473
OY	414	DYRSGYDKNVOMLADYTFIMSPFGATLIMLVNFEGLALCKMHNHAILKPPSGCLD	473
DB	2662	DPEGGNDPCWISIHBPILMSPAGPIVLYVNGI-----MFLAARTSCSTGORE	2713
OY	474	NIKSMVI-----GATALLCLGLTFAWGLAMYNESYIMAYLFETIFNSLOGMFIFFHCVL	529
DB	2714	AKRTSVLRTLRSSPLDLLLVASMLGGLLANVNSVLAFFHYHAGLOGGLAVLLFCVL	2773
OY	530	QKKYRKREYGCILRTHCCSGKSTESSIGSGTKSGSRTPGRYSTGOSOSIRRMNDTVRKOS	589
DB	2774	NADRAAW-----TPACLGKRAPE-----ETRAPAPGP-----	2802
OY	590	ESSFTGDISNSASLANEGILNNAPDTSWDTL-PLNCHNGNSYSIAGEYLSNCYII	647
DB	2803	-----SGAVNYNTALFEESGILRTTLGASTVSSVSARSRGADODOSRGSRSLRNVLV-	2856
OY	648	DRGYNHMETALEKKILKELTSNYIPSYLNHRRSSQONLNMKLVNNGSGREDADYVL	707
DB	2857	-----RHGSTA-----EHAENSLQAHAPDTLDVAMHR-----DACADSDS---	2892
OY	708	DDATSPNHSSLSGLLEIHEESDA-----PLLPVRYSTENHOPHYTRRRIPQDSE	759
DB	2894	DSDSLSEERSLSPISSESEDNRTGRFORPL--RRAQSEKILAH-----PKVDVG	2944
OY	760	-----SFPPL-----TNEHTEDLOSPPHDSLYTSMPTLACVATES	796
DB	2945	NDLISYWPALGCEBAPCALQANGSERRLGDS-NKDAANNOPELATLSGDET	2997
RESULT 11			
CLR3_MOUSE			
ID	CLR3_MOUSE	STANDARD;	PRT; 3301 AA.
AC	O91ZIO; Q9ESD0;		
DT	15-JUN-2002 (Rel. 41, Created)		
DT	15-JUN-2002 (Rel. 41, Last sequence update)		
DT	15-JUN-2002 (Rel. 41, Last annotation update)		
DE	Cadherin EGF LAG seven-pass G-type receptor 3 precursor.		
GN	CELSR3.		
OS	Mus musculus (Mouse).		
OC	Eukaryota; Metazoa; Chordata; Cranata; Vertebrata; Euteleostomi;		
OC	Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Mus.		
OX	NCBI.Taxid=10090;		
RN	[1]		
RP	SEQUENCE FROM N.A., AND DEVELOPMENTAL STAGES.		
RC	STRAIN=C57BL/6;		
RC	PUMed=11850187;		
RA	Tissir F., De-Backer O., Goffinet A.M., Lambert de Rouvroit C.A.;		
RA	"The flamingo-related mouse Celser family (Celsr1-3) genes exhibit		
RT	distinct patterns of expression during embryonic development.";		
RL	Mech. Dev. 112:157-160(2002).		
RN	[2]		
RN	SEQUENCE OF 2574-3046 FROM N.A., AND DEVELOPMENTAL STAGE.		
RP	PUMed=11677057;		
RX	Formstone C.J., Little P.F.R.;		
RA	"The flamingo-related mouse Celser family (Celsr1-3) genes exhibit		
RT	distinct patterns of expression during embryonic development.";		
RL	Mech. Dev. 109:91-94(2001).		
RN	[3]		
RP	TISSUE SPECIFICITY.		
RX	PUMed=10790539;		
RA	Formstone C.J., Barclay J., Rees M., Little P.F.R.;		
RA	"Candidate for the lippy (lip) lethal mutant on chromosome 9.";		
RT	Mamm. Genome 11:392-394(2000).		
CC	-1- FUNCTION: Receptor that may have an important role in cell/cell		
CC	signaling during nervous system formation.		
CC	-1- SUBCELLULAR LOCATION: Integral membrane protein.		
CC	-1- TISSUE SPECIFICITY: Expressed in the CNS and in the eye.		
CC	-1- DEVELOPMENTAL STAGE: Predominantly expressed in the CNS, the		
CC	emerging dorsal root ganglia and cranial ganglia. In the CNS,		
CC	expression is uniform along the rostrocaudal axis. No expression		
CC	is detected until somite stages. Between E10 and E12, expression		

CC	is strong in the marginal zone (MZ), and lower in the ventricular zone (VZ). At E15, expression is restricted to the brain and olfactory epithelium. In the brain, it is low in VZ but strong in external fields, particularly those with ongoing migration, such as the telencephalic cortical plate, the olfactory bulb, the cerebellum and the tectum. In the newborn and postnatal stages, expression is high in differentiated neuronal fields.
CC	-1 SIMILARITY: BELONGS TO FAMILY 2 OF G-PROTEIN COUPLED RECEPTORS.
CC	-1 SIMILARITY: CONTAINS 9 CADHERIN DOMAINS.
CC	-1 SIMILARITY: CONTAINS 7 EGF-LIKE DOMAINS.
CC	-1 SIMILARITY: CONTAINS 2 LAMININ G-LIKE DOMAINS.
CC	-1 SIMILARITY: CONTAINS 1 LAMININ EGF-LIKE DOMAIN.
CC	-1 SIMILARITY: CONTAINS 1 GPS DOMAIN.
CC	-1 CAUTION: Ref 2 sequence differs from that shown due to frameshifts in positions 2575 and 2578.
CC	-----
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CC	-----
DR	EMBL; AF427498; AAL25099.1; -
DR	EMBL; AF188752; AAG17057.1; ALT_FRAME.
DR	MGI; MGI:1858236; Celsr3.
DR	InterPro: IPR000152; Asx_hydroxyl.
DR	InterPro: IPR002126; Cadherin.
DR	InterPro: IPR000561; EGF-like.
DR	InterPro: IPR000742; EGF_2.
DR	InterPro: IPR000832; GPCR_secretin.
DR	InterPro: IPR001879; hormn_receptor.
DR	InterPro: IPR002049; laminin_EGF.
DR	InterPro: IPR001791; laminin_G.
DR	InterPro: IPR000203; PKD_cys-rich.
DR	Pfam; PF00002; 7tm_2; 1.
DR	Pfam; PF00028; cadherin; 9.
DR	Pfam; PF00008; EGF; 6.
DR	Pfam; PF01825; GPS; 1.
DR	Pfam; PF02793; HRM; 1.
DR	Pfam; PF00054; laminin_G; 2.
DR	PROSITE; PS00010; ASX_HYDROXYL; 1.
DR	PROSITE; PS00232; CADHERIN_1; 7.
DR	PROSITE; PS50268; CADHERIN_2; 8.
DR	PROSITE; PS00022; EGF_1; 5.
DR	PROSITE; PS01186; EGF_2; 4.
DR	PROSITE; PS01248; LAMININ_TYPE_EGF; 1.
DR	PROSITE; PS50221; GPS; 1.
DR	PROSITE; PS50025; LAM_G_DOMAIN; 2.
DR	PROSITE; PS00649; G_PROTEIN_RECPE_F2_1; FALSE_NEG.
DR	PROSITE; PS00650; G_PROTEIN_RECPE_F2_2; FALSE_NEG.
DR	PROSITE; PS50227; G_PROTEIN_RECPE_F2_3; 1.
DR	PROSITE; PS50261; G_PROTEIN_RECPE_F2_4; 1.
KM	G-protein coupled receptor; Transmembrane; Glycoprotein;
KM	EGF-like domain; Calcium-binding; Laminin EGF-like domain; Repeat;
KM	Developmental protein; Hydroxylation; Signal.
FT	SIGNAL 1 31
FT	POTENTIAL.
FT	CHAIN 32 3301
FT	CADHERIN EGF LAG SEVEN-PASS G-TYPE
FT	RECEPTOR 3.
FT	DOMAIN 32 2531
FT	EXTRACELLULAR (POTENTIAL).
FT	TRANSSEM 2532 2552
FT	1 (POTENTIAL).
FT	DOMAIN 2553 2563
FT	CYTOPLASMIC (POTENTIAL).
FT	TRANSSEM 2564 2584
FT	2 (POTENTIAL).
FT	DOMAIN 2585 2592
FT	EXTRACELLULAR (POTENTIAL).
FT	TRANSSEM 2593 2613
FT	3 (POTENTIAL).
FT	DOMAIN 2614 2634
FT	CYTOPLASMIC (POTENTIAL).
FT	TRANSSEM 2635 2655
FT	4 (POTENTIAL).
FT	DOMAIN 2656 2673
FT	EXTRACELLULAR (POTENTIAL).
FT	TRANSSEM 2674 2694
FT	5 (POTENTIAL).
FT	DOMAIN 2695 2716
FT	CYTOPLASMIC (POTENTIAL).
FT	TRANSSEM 2717 2737
FT	6 (POTENTIAL).
FT	DOMAIN 2738 2744
FT	EXTRACELLULAR (POTENTIAL).

Query Match	Best Local Match	Similarity	Score	DB	Length
47	NCAMETVNNLLPOLANWRDL--TTSDDLRATMTLHVEESAFVLADNLKTDI--	101	11.4%	518.5	3301
Matches 194;	Conservative 132;	Mismatches 337;	Indels 167;	Gaps 28;	

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Db 2247 NENLLMAGSALLALETGHLMALQORAPGSGSAGLVQH-LEBYAATLARNMELTYLNP 2305
OY 102 VRENTDNKLEVARL-----STEGNLEDEKPEPENNCHG-----S 135
Db 2306 VGLVTPNIMLSIDNMEHBSSTOGARRPRYHNSLFRGODANDPHTHVLPSQASOPSPSE 2365
OY 136 TIOLASANT-----LKONGRCEIRAFVLYNNIGPYLSTENASMKLGTAL 181
Db 2366 VLPTSSNENATASSVSPAPRLEPESPISIVILLYRALGGLPQOAEKRGAR- 2423
OY 182 STNSVIVNSVYTAALINKESNMKYVLADPVYTVK---HIKQSEENPNPCSWTSKR 238
Db 2424 -LPONPWNSPVVAV--FHGRNPLRGVLYVSPINEEFRLQYANRSKATCYQMDPPGP 2479
OY 239 T-MGYVSTOGCRLLTNTKTHHTSCNHLTFEAVLMAHVEKHSADAVDL-LDVIYVWG 296
Db 2480 TDQNGMWTARCELVHRNGSHARCSRCTGTGYLMDASPERLEBG--DELLAVFTHV 2537
OY 297 ILLSLVCLLICIFTECFEFGIQSDRNTIHKMLCISLFAVELLFIQINRTDQPIACAVFA 356
Db 2538 VAVSVTALVTAVALLSIRSLKSNVRGIHANVAALGAVALLELLGIHRTNQLCTAVA 2597
OY 357 ALLHFFPLAATMFLBEVQIYIMLVEFESEHSRRKFTYVGYGMPALIYAASANDYR 416
Db 2598 ILLHYFLSTFAMLLVOGLHLYRMQVEPRNDRGAMREYHAIQGVPAVLLGLAVGLDPE 2657
OY 417 SYGDKCWLRLDYTFIWSFGPATLIIMLVFIQIYALYKMFHHTALPKESGLDNK 476
Db 2658 GYGNPDCWISIHPLINSFPGIYLYLVAN-----GIMFLAARTSCSTGOREAKK 2709
OY 477 SWVI--GAIALCLGLGTMAFGMYINESTVIMAYLETTIPNSLOGMEFIHCVLOKKV 533
Db 2710 TSVLTIRSSFFLLLVASWIFGLAVNHSILAFHYLAGCGIQLAVLLFLFCVLNDA 2769
OY 534 RKEGKCLRTCCSGKSTRESSIGSGKTSGRTPGRYTSQSRIIRMANNDYRKQSESEF 593
Db 2770 RAAV-----TPACLGKKAAP-----ETRPAPGP----- 2794
OY 594 ITGDISSASINREGILNNAARDVSMPTL--PLNGNHNCSYSIASGEYLSNCOYIDRG 651
Db 2795 -SGAYNNTALPEESGLIRITIGASTVSSVARSGRADODOSQGRSLRNVLV----- 2848
OY 652 NHNETALEKKILKEIYNSYIPSYLNHNRSEONRNMLKNLNLGSGREDDATVLDAT 711
Db 2849 RHGSTA-----EHTERSLOAHNAGPTDLVAMFHR-----DAGADSDS--DSDL 2889
OY 712 SFNHEESIGLELHEBSA-----PLPFRVYSTENHOPHHYTRRRITQDHS----- 759
Db 2890 SLEBERSLSTSSSESDNGRTGRFORPL--RAAQSERLLAH-----PKDVGNDL 2940
OY 760 SFFPL-----TNEHTEDLOSPHRDSLYTSMPTAGVAATES 796
Db 2941 SYWALGECBAAPCALQAMGSERLGLDS-NKDAANNQPELALUTSGDET 2989

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RESULT 12
CLR3_HUMAN
ID CLR3_HUMAN STANDARD; PRT; 3312 AA.
AC 09NTQ7; 075092;
DT 15-JUN-2002 (Rel. 41, Created)
DT 15-JUN-2002 (Rel. 41, Last sequence update)
DE 15-JUN-2002 (Rel. 41, Last annotation update)
DE Cadherin EGF lag seven-pass G-type receptor 3 precursor (Flamingo
DE homolog 1) (hfm1) (Multiple epidermal growth factor-like domains 2)
DE (Epidermal growth factor-like 1).
GN CELSR3 OR COH1L OR FM1L OR EGFL OR MEGF2.
OS Homo sapiens (Human).
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC Mammalia; Eutheria; Primates; Catarrhini; Homnidae; Homo.
OX NCBI_TaxID=9606;
RN [1]
SEQUENCE FROM N.A.

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RX MEDLINE=20202599; PubMed=10716726;
RA Wu Q., Maniatis T.;
RT "Large exons encoding multiple ectodomains are a characteristic
RT feature of protocadherin genes.";
RL Proc. Natl. Acad. Sci. U.S.A. 97:3124-3129(2000).
RN [2]
RP SEQUENCE OF 1954-3312 FROM N.A.
RC TISSUE=Brain;
RX MEDLINE=98360089; PubMed=9693030;
RA Nakayama M., Nakajima D., Nagase T., Nomura N., Seki N., Ohara O.;
RT "Identification of high-molecular-weight proteins with multiple
RT EGF-like motifs by molif-trap screening.";
RL Genomics 51:27-34(1998).
CC -1- FUNCTION: Receptor that may have an important role in cell/cell
CC signaling during nervous system formation.
CC -1- SUBCELLULAR LOCATION: Integral membrane protein.
CC -1- SIMILARITY: BELONGS TO FAMILY 2 OF G-PROTEIN COUPLED RECEPTORS.
CC -1- SIMILARITY: CONTAINS 9 CADHERIN DOMAINS.
CC -1- SIMILARITY: CONTAINS 8 EGF-LIKE DOMAINS.
CC -1- SIMILARITY: CONTAINS 2 LAMININ G-LIKE DOMAINS.
CC -1- SIMILARITY: CONTAINS 1 LAMININ EGF-LIKE DOMAIN.
CC -1- SIMILARITY: CONTAINS 1 GPS DOMAIN.
CC -----
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CC -----
DR EMBL; AF231023; AAF61929.1; -
DR EMBL; AB011536; BAA32464.1; -
DR HSSP; P00740; IEDM.
DR Genew; HGNC:3230; CELSR3.
DR MIM; 604264; -
DR InterPro; IPR000152; Asx_hydroxyl.
DR InterPro; IPR002126; Cadherin.
DR InterPro; IPR000561; EGF-like.
DR InterPro; IPR000742; EGF 2.
DR InterPro; IPR001881; EGF Ca.
DR InterPro; IPR000832; GPCR_secretin.
DR InterPro; IPR001879; hormn_receptor.
DR InterPro; IPR002049; Laminin_EGF.
DR InterPro; IPR001791; Laminin_G.
DR InterPro; IPR000203; PKD_cys_rich.
DR Pfam; PF00002; 7tm_2; 1.
DR Pfam; PF00028; cadherin; 9.
DR Pfam; PF00008; EGF; 6.
DR Pfam; PF01825; GPS; 1.
DR Pfam; PF02793; HRM; 1.
DR Pfam; PF00054; laminin_G; 2.
DR PRINTS; PR00249; GPCRSECRETIN.
DR PRINTS; PR00011; EGF_LAMININ.
DR SMART; SM00112; CA; 8.
DR SMART; SM00180; EGF_Lam; 1.
DR SMART; SM00001; EGF_like; 6.
DR SMART; SM00303; GPS; 1.
DR SMART; SM00008; Hormr; 1.
DR SMART; SM00282; Lamc; 2.
DR PROSITE; PS00010; ASX_HYDROXYL; 1.
DR PROSITE; PS00232; CADHERIN_1; 7.
DR PROSITE; PS50268; CADHERIN_2; 8.
DR PROSITE; PS00022; EGF_1; 6.
DR PROSITE; PS01186; EGF_2; 4.
DR PROSITE; PS50221; GPS; 1.
DR PROSITE; PS00649; G_PROTEIN_RECPR_F2_1; FALSE_NEG.
DR PROSITE; PS00650; G_PROTEIN_RECPR_F2_2; FALSE_NEG.
DR PROSITE; PS50227; G_PROTEIN_RECPR_F2_3; 1.
DR PROSITE; PS50261; G_PROTEIN_RECPR_F2_4; 1.
DR PROSITE; PS50025; LAM_G_DOMAIN; 2.
DR PROSITE; PS01248; LAMININ_TYPE_EGF; 1.

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[illegible]

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Db 3037 LGHRAVPAASGYHAGGTGTSQSPASRYSSEQLDLRLRQLSRRLREAPAPVLRPL 3096
QY 736 -RYVSE-----NHQPHHYTRRIPOHSEFFPLTNHEHEDQSPHSDLYT 783
Db 3097 SRGSGCCMDAPGRLEPPKRGSTLPRKPPRPGMACRFGSRDALDAP-REWLST 3155
QY 784 SMPTLAGVAATESYVSTQTEPPAKGD---AEDYVYKSM-----NLGSRNHVHQL 833
Db 3156 LPPRR-----TRLDQPPPLPLSPQLSRDLPLSRPLSLSRSSNSRDLQDY 3207
QY 834 HTYYQLGRSSDGFIVPNKDGTPP-----EGSSKGPAN 867
Db 3208 PSRH-----PSREALGPLQLLRAREDSVSGPSH 3236

RESULT 13
BA12_HUMAN
ID BA12_HUMAN STANDARD: PRT; 1572 AA.
AC 060241;
DT 16-OCT-2001 (Rel. 40, Last sequence update)
DT 16-OCT-2001 (Rel. 40, Last sequence update)
DT 15-JUN-2002 (Rel. 41, Last annotation update)
DE Brain-specific angiogenesis inhibitor 2 precursor.
GN BA12.
OS Homo sapiens (Human).
OC Eukaryota; Metazoa; Chordata; Vertebrata; Euteleostomi;
OC Mammalia; Eutheria; Primates; Catarrhini; Homnidae; Homo.
OX NCBI_TaxID=9606;
RN [1]
RP SEQUENCE FROM N.A.
RC TISSUE=Fetal brain;
RA MEDLINE=98194217; Pubmed=9533023;
RX Shitouchi T., Nishimori H., Ichise H., Nakamura Y., Tokino T.;
RT Cloning and characterization of BA12 and BA13, novel genes homologous
RL Cytochrome C. Cell Genet. 79:103-108(1997).
CC - FUNCTION: MIGHT BE INVOLVED IN ANGIOGENESIS INHIBITION.
CC - SUBCELLULAR LOCATION: Integral membrane protein.
CC - TISSUE SPECIFICITY: STRONGLY EXPRESSED IN BRAIN. ALSO DETECTED IN
CC HEART, THYMUS, SKLETERAL MUSCLE, AND DIFFERENT CELL LINES.
CC - SIMILARITY: BELONGS TO FAMILY 2 OF G-PROTEIN COUPLED RECEPTORS.
CC - SIMILARITY: CONTAINS 4 TSP TYPE-1 DOMAINS.
CC - SIMILARITY: CONTAINS 1 GPS DOMAIN.
CC
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CC or send an email to license@isb-sib.ch).
CC
DR EMBL: AB005298; BAA25362.1; -.
DR Genew: HGNC:944; BA12.
DR MIM: 602683; -.
DR InterPro: IPR000833; GPCR_secretin.
DR InterPro: IPR000203; PKD_cys_rich.
DR InterPro: IPR000884; TSP1.
DR InterPro: IPR001879; horma_receptor.
DR Pfam: PF00002; 7tm_2; 1.
DR Pfam: PF00090; tsp_1; 4.
DR Pfam: PF01825; GPS_1.
DR Pfam: PF02793; HRM; 1.
DR SMART: SM00303; GPS; 1.
DR SMART: SM00008; HORMR; 1.
DR SMART: SM00209; TSP1; 4.
DR PROSITE: PS50221; GPS; 1.
DR PROSITE: PS00649; G_PROTEIN_RECP_F2_1; FALSE_NEG.
DR PROSITE: PS00650; G_PROTEIN_RECP_F2_2; FALSE_NEG.
DR PROSITE: PS50227; G_PROTEIN_RECP_F2_3; 1.
DR PROSITE: PS50261; G_PROTEIN_RECP_F2_4; 1.
DR PROSITE: PS50092; TSP1; 4.

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KW G-protein coupled receptor; Transmembrane; Glycoprotein; Signal;
Repeat.
FT SIGNAL. 1 20
FT CHAIN. 21 1572
FT DOMAIN. 21 924
FT TRANSSEM. 925 945
FT TRANSSEM. 946 953
FT TRANSSEM. 954 974
FT TRANSSEM. 975 982
FT TRANSSEM. 983 1003
FT TRANSSEM. 1004 1024
FT TRANSSEM. 1025 1045
FT TRANSSEM. 1046 1066
FT TRANSSEM. 1067 1087
FT TRANSSEM. 1088 1141
FT TRANSSEM. 1142 1162
FT TRANSSEM. 1163 1189
FT TRANSSEM. 1169 1189
FT TRANSSEM. 1190 1572
FT TRANSSEM. 1297 351
FT TRANSSEM. 352 406
FT TRANSSEM. 407 461
FT TRANSSEM. 463 517
FT TRANSSEM. 859 911
FT TRANSSEM. 117 122
FT TRANSSEM. 177 180
FT TRANSSEM. 222 225
FT TRANSSEM. 1303 1305
FT TRANSSEM. 1352 1358
FT TRANSSEM. 1413 1418
FT TRANSSEM. 94 94
FT TRANSSEM. 179 179
FT TRANSSEM. 180 180
FT TRANSSEM. 344 344
FT TRANSSEM. 425 425
FT TRANSSEM. 548 548
FT TRANSSEM. 633 633
FT TRANSSEM. 855 855
FT TRANSSEM. 1572 AA; 171140 MW; A975645877BC285 CnC64;
SO SEQUENCE

Query Match 11.18; Score 505.5; DB 1; Length 1572;
Best Local Similarity 21.88; Pred. No. 7.7e-25;
Matches 233; Conservative 146; Mismatches 347; Indels 345; Gaps 44;

QY 10 AGDITVSRAVDLVGLDYDLVLRNL-----PGKDSAAKSLKAWETVNNLLQP 60
Db 621 SGDLFEV-----DI-LRNVDTFKRATVYPADV-----QRFQVVSFWDA 663
QY 61 QALNARDLTTSDQLRATM-LHTEV-----ESAFVLADNL----- 97
Db 664 ENKEKMD--AQVSPGSVHLRVEDEFLVGDALKAFQSSLIYVDNLVISIOPRVS 720
QY 98 -----KDIYRENTDNKL--EVARLSTEGULDEL-----KF 127
Db 721 AVSSDITFPKRGKGMKQWVHSEDRLEFLPREVLSLSPGAPATSGAAGSFGRGPGTV 780
QY 128 PENNGHSTIOLISANTLKONGRNGEIRVAFVLYNNLGPYSTENASMKLGTALSTNHSV 187
Db 781 PRGCHSHQRLRPADP-----DESSYFVIGAVLYTTLGLILPPRPPL----- 823
QY 188 IVNSPVITAAINKESKNVYIADPVFTVKHIKSEENFNPNCSFWSYSKR-TWTGWST 246
Db 824 AVTSRVMTVVRPPTPP--AEPLI-TVELSYIINGTTPPHCASMPYSRADSSSGMDT 879
QY 247 QGCRLLTNTKHTTGCSCNHLNFAVLAHVEVKSADAVHDLIDVITWVGLISVCLLI 306
Db 880 ENCQTLETAATRCQCOHSTFAVL-----AQPCKDITLTLAAGSPVLYIGCAVS 931
QY 307 CTFTE-----CFRGLSDRNTIHKNLCSLFEVAFLEFGINRTDQPIACAVFALL 359
Db 932 CMALLTILAIYAAPWRFKRSRSTIILNFCILIASNILLVQGSRYLSKGYCMTAAFL 991
QY 360 HFFFLAAFTWMLFEGVOLYIMLVEFESEHSRRRYFVLGVGMDALIVAVSAA-VDYRSY 418

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FT SITE 231 233 CELL ATTACHMENT SITE (POTENTIAL).
 FT DOMAIN 1365 1584 NECESSARY FOR INTERACTION WITH BAP1.
 FT 1581 1584 INDISPENSABLE FOR INTERACTION WITH BAP1.
 FT CAROHD 64 64 N-LINKED (GLCNAC. . .) (POTENTIAL).
 FT CAROHD 401 401 N-LINKED (GLCNAC. . .) (POTENTIAL).
 FT CAROHD 607 607 N-LINKED (GLCNAC. . .) (POTENTIAL).
 FT CAROHD 692 692 N-LINKED (GLCNAC. . .) (POTENTIAL).
 FT CAROHD 844 844 N-LINKED (GLCNAC. . .) (POTENTIAL).
 FT CAROHD 877 877 N-LINKED (GLCNAC. . .) (POTENTIAL).
 FT CAROHD 881 881 N-LINKED (GLCNAC. . .) (POTENTIAL).
 SQ SEQUENCE 1584 AA: 173531 MM: DEABF28C7874513 CRC64;

Query Match 10.9%; Score 496.5; DB 1; Length 1584;
 Best Local Similarity 25.5%; Pred. No. 36-24;
 Matches 175; Conservative 123; Mismatches 268; Indels 121; Gaps 32;

OY 3 QRRNHADITYSVARMOVLVDOLRL-----TPGKSAASLKAW 51
 DB 667 QRLVEISQDGTYS---GDLLSTIDV-LRNMTETFRAYSPEDDVON-----FV 713
 OY 52 ETVNNLLQPOLNARMDLTTSDQLRA--ATMLHTVEESAFVLADNLKTDIYRENTDI 109
 DB 714 QILSNLAEENRDKWEA---QLAGPNKELFRLVEDFVDFGPMKDLRDAYQYTDNL 769
 OY 110 KLEVARLSTEGNLEDLKPEPNMGHS-----TQLS--ANTLQNGRNGEIRVA 156
 DB 770 VLSIHLPLPASG--ATDISFPMKGWRATGMAKVEDEHVTYSKVSFGLTEADBSAFVVG 828
 OY 157 FVLYNNLGPYLSTENASMLGTALSTNHSVYNVITAIKESNKKVYLADPVVTV 216
 DB 829 TVLYRNLGSLAQ-----RNTTVNSKVISTVAPPPRS---LRTPLEIEF 872
 OY 217 KHIQSEENFPNCSFW-----SYSKRTWTGYSTQGCRLTNTKTHTCNSHLTNEFA 270
 DB 873 AHMYNG--TTCNCILMDELDVPSASAPQLGPMWRCGTVDLRLTRCLODRISTFA 930
 OY 271 VLM-----AHVEVKSDAVHDLIDVITWVGIILSVCLLICITFCFGRGLOSDRNTIH 325
 DB 931 IIAQLSADANMERATLPV---TLIVGCV--SLTLMLLVITVYVSWRYIRSESVIL 984
 OY 326 KNCISLFAVELLFLGINTDPIACAVPALHFEFLAFLMFLLEGVQLTLMLEVEF 385
 DB 985 INCLSIISNALLITIGOTQTRNKVKCTLVAALHFEFLSSFCWVLTETAMQSTMAV--- 1040
 OY 386 ESEHSR-----RKTYLVGVGMPALIAVNSA--DYRSYGTDKCMLRLDTYTFSEFIPA 440
 DB 1041 -TGHNLRLIRKRFCLGMLPALVAISGFCFKAGYSMTNMCMLTBEGGLIYAVGPA 1099
 OY 441 TLIIMLVITFLGIALY-KMFHTAT---LKPSGCLDNITKSVIGALIALCLGLTWAF 495
 DB 1100 AAVVLYNMV-IGILVFNKLVSKDGIIDDKLKERAGA---SLW--SSCVVLPPLATWMS 1152
 OY 496 GLMYTME-STVIWAYLFTTFNSLOGMFIFFHCVLOKVKYKCKLCRTCCSGKSTRESS 554
 DB 1153 AVLAATVDRNSALFQILFAVFDSEGFYIYVWHLIKREV-QDVVKCRV-----DROE 1204
 OY 555 IGSQSGSKRTPS--RYSYTSQSRIRRMNDYTRKO---SESSFITGINSASLNRGL 609
 DB 1205 EGGDGGGSGNQNHQALMDTFEDKVDVLACGSYVKNKIDACRTATITIGTLKRPSPBEK 1264
 OY 610 -LNNARDTSV-MDTPLNGN---HGN 630
 DB 1265 KLAHAKGPTNFNSLPAVNSKHLHGS 1291

RESULT 15
 STAN_DROME STANDARD; PRT: 3579 AA.
 AC 09V5N8;
 DT 15-JUN-2002 (Rel. 41, Created)
 DT 15-JUN-2002 (Rel. 41, Last sequence update)
 DT 15-JUN-2002 (Rel. 41, Last annotation update)
 DE Protocadherin-like wing polarity protein stan precursor (starry night

DE protein) (Flamingo protein).
 GN STAN OR FMI OR CG11895.
 OS Drosophila melanogaster (Fruit fly).
 OC Eukaryota; Metazoa; Arthropoda; Mandibulata; Pancrustacea; Hexapoda;
 OC Insecta; Pterygota; Neoptera; Endopterygota; Diptera; Brachyera;
 OC Muscomorpha; Ephydroidea; Drosophilidae; Drosophila.
 OX NCBI_Taxid=7227;
 RN [1]
 RP SEQUENCE FROM N.A., FUNCTION, TISSUE SPECIFICITY, AND DEVELOPMENTAL
 RP STAGE.
 RC TISSUE=Embryo;
 RX MEDLINE=20025940; PubMed=10556066;
 RA Chae J.W., Kim M.-J., Goo J.H., Collier S., Gubb D., Charlton J.,
 RA Adler P.N., Park W.J.;
 RT "The Drosophila tissue polarity gene starry night encodes a member of
 RT the protocadherin family.";
 RL Development 126:5421-5429(1999).
 RN [2]
 RP SEQUENCE FROM N.A., FUNCTION, AND SUBCELLULAR LOCATION.
 RX MEDLINE=99418630; PubMed=10490098;
 RA Usui T., Shima Y., Shimada Y., Hirano S., Burgess R.W., Schwarz T.L.,
 RA Takeichi M., Demura T.;
 RT "Flamingo, a seven-pass transmembrane cadherin, regulates planar cell
 RT polarity under the control of frizzled.";
 RL Cell 98:585-595(1999).
 RN [3]
 RP SEQUENCE FROM N.A.
 RC STRAIN=Berkely;
 RX MEDLINE=20196006; PubMed=10731132;
 RA Adams M.D., Celisner S.E., Holt R.A., Evans C.A., Gocayne J.D.,
 RA Amanatides P.G., Scherer S.E., Li P.W., Hoskins R.A., Galle R.F.,
 RA George R.A., Lewis S.E., Richards S., Ashburner M., Henderson S.N.,
 RA Sutton G.G., Mortman J.R., Yandell M.D., Zhang Q., Chen L.X.,
 RA Brandon R.C., Rogers Y.-H.C., Blazer R.G., Champe M., Pfeiffer B.D.,
 RA Wan K.H., Doyle C., Baxter E.G., Helt G., Nelson C.R., Miklos G.L.G.,
 RA Abril J.F., Agbayani A., An H.-J., Andrews-Franckoch C., Baldwin D.,
 RA Baller R.M., Basu A., Baxendale J., Bayraktaroglu U., Beasley E.M.,
 RA Beeson K.Y., Benos P.V., Berman B.P., Bhandari D., Bolshakov S.,
 RA Borzova D., Botchan M.R., Bouck J., Brokstein P., Brotlier P.,
 RA Burris J.C., Busam D.A., Butler H., Cadieu E., Center A., Chandra I.,
 RA Chertys K.M., Cawley S., Dahlke C., Davenport L.B., Davies P.,
 RA de Pablo B., Delcher A., Deng Z., Mays A.D., Dew I., Dietz S.M.,
 RA Dodson K., Doup L.E., Downes M., Dugan-Rocha S., Dunkov B.C., Dunn P.,
 RA Durbin K.J., Evangelista C.C., Ferraz C., Ferreira S., Fleischmann W.,
 RA Flosser C., Gabrielian A.E., Gary N.S., Gelbart M.M., Glasser K.,
 RA Gosdek A., Gong F., Gorrell J.H., Gu Z., Guan P., Harris M.,
 RA Harris N.L., Harvey D., Helman T.J., Hernandez J.R., Houck J.,
 RA Hostin D., Houston K.A., Howland T.J., Mel M.-H., Ibegwam C.,
 RA Jatali M., Kalush F., Karpen G.H., Ke Z., Kennison J.A., Ketchum K.A.,
 RA Kimmel B.E., Kodira C.D., Kraft C., Kravitz S., Kulp D., Lai Z.,
 RA Lasko P., Lei Y., Levitsky A.A., Li J., Li Z., Liang Y., Lin X.,
 RA Liu X., Mattei B., McIntosh T.C., McLeod M.P., McPherson D.,
 RA Merkulov G., Mishina N.Y., Mobarry C., Morris J., Moshrefi A.,
 RA Mount S.M., Moy M., Murphy B., Murphy L., Muzny D.M., Nelson D.L.,
 RA Nelson D.R., Nelson K.A., Nixon K., Nusslein D.R., Pacleb J.M.,
 RA Palazolo M., Pittman G.S., Pan S., Pollard J., Puri V., Reese M.G.,
 RA Reibert K., Remington K., Saunders R.D.C., Scheeler F., Shen H.,
 RA Shue B.C., Siden-Kiamos I., Simpson M., Skupski M.P., Smith T.,
 RA Spier E., Spradling A.C., Stapleton M., Strong R., Sun E.,
 RA Szyrkas R., Tector C., Turner R., Venter E., Wang A.H., Wang X.,
 RA Wang Z.-Y., Wasserman D.A., Weinstein G.M., Weisenbach J.,
 RA Williams S.M., Woodage T., Worley K.C., Wu D., Yang S., Yao Q.A.,
 RA Ye J., Yeh R.-F., Zaveri J.S., Zhan M., Zhang G., Zhao Q., Zheng L.,
 RA Zheng X.H., Zhong F.N., Zhong W., Zhou X., Zhu S., Zhu X., Smith H.O.,
 RA Gibbs R.A., Myers E.W., Rubin G.M., Venter J.C.;
 RT "The genome sequence of Drosophila melanogaster.";
 RL Science 287:2185-2195(2000).
 CC -1- FUNCTION: Involved in the fz signaling pathway that controls wing
 CC tissue polarity. Also mediates homophilic cell adhesion. May play
 CC a role in initiating prehair morphogenesis. May play a critical
 CC role in tissue polarity and in formation of normal dendrite
 CC fields.
 CC -1- SUBCELLULAR LOCATION: Integral membrane protein.


```

OY 387 SEHSRRRYEYIVGVGMALLIVAAVSAANDVRSQYDCKVCLRLDTYFINSFGLPATLIML 446
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Db 2914 INHPRMGFYPMAGYGAPAIIVGSLVGYRAHEHNGNSJFCWLSYEPVVMWVLGPILAGKSIV 2973
OY 447 NVIFELGIALYKMFHHTPAILPESGCDLNKSWVIGAILALCLLGLTMAFGMIYNESVI 506
      | : : : : : : : : : : : : : : : : : : : : : : : : : : : : : :
Db 2974 NLLILFVSXAAE----TLKDHWLGFGRNRTLLMLSVSLPLMGVMWVLAVLASEHSQ 3029
OY 507 MAYLFTFNSLQGMFIFIFHCYLQCKVREYEG-CLTHCSGK----- 549
      | : : : : : : : : : : : : : : : : : : : : : : : : : : : : : :
Db 3030 LSLILSGVLLHALFCLIGCIINKRRENLRTCLDR--CMGRVPLDSSMVSNSH 3086
OY 550 -----STESSIG-SGKTSGRGRYSTG--SQSRIRMMNDYVKQ 588
      | : : : : : : : : : : : : : : : : : : : : : : : : : : : : : :
Db 3087 NVNNAARPNFLASGYITTRRNIGTSASSTTSRSTAKTSSPYDGOJRGSTISYVN 3146
OY 589 SES---SFITGDISSASLNREGLLNANDSYMOTPLPNGHGSYSIASGEYSLNCVQ 645
      | : : : : : : : : : : : : : : : : : : : : : : : : : : : : : :
Db 3147 SASDAPFELGFEESTYGRSGRGEKPSR-RQRKSDSGSEYDGRSLDELASHSSDDDES 3205
OY 646 IIDRGY-NHNETALEKILKELTSNTPSYLNNHERSSQONNL-----MNKLY-- 693
      | : : : : : : : : : : : : : : : : : : : : : : : : : : : : : :
Db 3206 RTARSSGSTRSTAVSS-----TPALPNITEHYOATTPPELVVQOSPOLPEPVAKPYVA 3259
OY 694 -----NVLGSGREDALIVLDATSFNHEHSLLELILHE-----SDAPLL 733
      | : : : : : : : : : : : : : : : : : : : : : : : : : : : : : :
Db 3260 PRMSSQLPDALVLOSPNIGMSOD-----TGSNHE-----VHOAKMTISPNLP 3305
OY 734 PPRVYSTEHQPHHYTRRRIRPDHSESFPFLPLTNEHTELOSPHRDSLY---TSMPTLAG 790
      | : : : : : : : : : : : : : : : : : : : : : : : : : : : : : :
Db 3306 NPDLDTSTYLOOH-----HNKINMPSELLENIRARRGYSDDLXGRGCEYPRKYG 3355
OY 791 VAATESYTTSTQTEPPRPAKCGDAEDVYYSMPNLGSRN---HVHQLH-----TYUQ 838
      | : : : : : : : : : : : : : : : : : : : : : : : : : : : : : :
Db 3356 -----SYKPPSHSGSEKD-----YEGGGSGSQTGHMSKSPHDAAYLSNDIYD 3398
OY 839 LGRSSSDGFIYVP-----NKDGTPE--GSSKG-----PAHLVYSL 872
      | : : : : : : : : : : : : : : : : : : : : : : : : : : : : : :
Db 3399 KQRLTSGGTYLGANSSESYLSKDDITPDYIGSRDGHYSLKROPAVATDUL 3447

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Search completed: December 10, 2002, 11:11:59
Job time : 48 secs

Db 340 SSECCELYTSENHTSCRNHLTHFAILMSSGSPSIGIKDYN-----ILTRITOLGIITSL 394
OY 302 VCLLICIFTCFPRGLQSDNRTIHKNCISLFEVALLFLGINFTDQPIACAVFAALLHF 361
Db 395 ICAICICFTFWFSEIOSTRTTIHKNCISLFEVALLFLGINFTDQPIACAVFAALLHF 454
OY 362 FFLAFTWMELEGVQYIMLVEFESESRKRYEYLVGYGMPALIVASAVDRSYGTD 421
Db 455 FFLAFAFMCMIEGHLHYVGVYVYKNGFLHKNFYIFGVLSPAVVGFSAALGRYGGT 514
OY 422 KVCMLRDTFIMSFIPALILMLNFIAGIALYKMFHTAILKPESGLDNIKSWVG 481
Db 515 KVCMLSTENNFIMSFIPALILMLNFIAGIALYKMFHTAILKPESGLDNIKSWVG 574
OY 482 AIALCLGLTMAFGLYNFIMSFIPALILMLNFIAGIALYKMFHTAILKPESGLDNIKSWVG 541
Db 575 AIALCLGLTMAFGLYNFIMSFIPALILMLNFIAGIALYKMFHTAILKPESGLDNIKSWVG 634
OY 542 R-THCCSG 548
Db 635 KNPCCCG 642

RESULT 2
US-09-905-291A-49
Sequence 49, Application US/09905291A
Patent No. US20020160374A1
GENERAL INFORMATION:
APPLICANT: Genentech, Inc.
APPLICANT: Ashkenazi, Avi
APPLICANT: Botstein, David
APPLICANT: Desnoyers, Luc
APPLICANT: Eaton, Dan L.
APPLICANT: Ferrara, Napoleone
APPLICANT: Filvaroff, Ellen
APPLICANT: Fong, Sherman
APPLICANT: Gao, Wei-Qiang
APPLICANT: Gerber, Hanspeter
APPLICANT: Gertlisen, Mary E.
APPLICANT: Goddard, A.
APPLICANT: Godowski, Paul J.
APPLICANT: Grimaldi, Christopher J.
APPLICANT: Gurney, Austin L.
APPLICANT: Hillan, Kenneth, J.
APPLICANT: Kijavlin, Ivar J.
APPLICANT: Mather, Jennie P.
APPLICANT: Pan, James
APPLICANT: Paoni, Nicholas F.
APPLICANT: Roy, Margaret Ann
APPLICANT: Stewart, Timothy A.
APPLICANT: Tumas, Daniel
APPLICANT: Williams, P. Mickey
APPLICANT: Wood, William, I.
TITLE OF INVENTION: Secreted and Transmembrane Polypeptides and Nucleic
FILE REFERENCE: 10466-14
CURRENT APPLICATION NUMBER: US/09/905,291A
CURRENT FILING DATE: 2001-07-12
PRIOR APPLICATION NUMBER: PCT/US00/04414
PRIOR FILING DATE: 2000-02-22
PRIOR APPLICATION NUMBER: US 60/143,048
PRIOR FILING DATE: 1999-07-07
PRIOR APPLICATION NUMBER: US 60/145,698
PRIOR FILING DATE: 1999-07-26
PRIOR APPLICATION NUMBER: US 60/146,222
PRIOR FILING DATE: 1999-07-28
PRIOR APPLICATION NUMBER: PCT/US99/20594
PRIOR FILING DATE: 1999-09-08
PRIOR APPLICATION NUMBER: PCT/US99/20944
PRIOR FILING DATE: 1999-09-13
PRIOR APPLICATION NUMBER: PCT/US99/21090
PRIOR FILING DATE: 1999-09-15

PRIOR APPLICATION NUMBER: PCT/US99/21547
PRIOR FILING DATE: 1999-09-15
PRIOR APPLICATION NUMBER: PCT/US99/23089
PRIOR FILING DATE: 1999-10-05
PRIOR APPLICATION NUMBER: PCT/US99/28214
PRIOR FILING DATE: 1999-11-29
PRIOR APPLICATION NUMBER: PCT/US99/28313
PRIOR FILING DATE: 1999-11-30
PRIOR APPLICATION NUMBER: PCT/US99/28564
PRIOR FILING DATE: 1999-12-02
PRIOR APPLICATION NUMBER: PCT/US99/28565
PRIOR FILING DATE: 1999-12-02
PRIOR APPLICATION NUMBER: PCT/US99/30095
PRIOR FILING DATE: 1999-12-16
PRIOR APPLICATION NUMBER: PCT/US99/30911
PRIOR FILING DATE: 1999-12-20
PRIOR APPLICATION NUMBER: PCT/US99/30999
PRIOR FILING DATE: 1999-12-20
PRIOR APPLICATION NUMBER: PCT/US00/00219
PRIOR FILING DATE: 2000-01-05
NUMBER OF SEQ ID NOS: 423
SEQ ID NO 49
LENGTH: 690
TYPE: PRT
ORGANISM: Homo sapiens
US-09-905-291A-49

Query Match 23.9%; Score 1088.5; DB 9; Length 690;

Best Local Similarity 41.4%; Pred. No. 1.5e-77;

Matches 227; Conservative 111; Mismatches 189; Indels 21; Gaps 11;

OY 8 LMAGDITYSVRAMDQVLGLDVLQRLNTPGKDSARSKNAVEYVNNLLOPALNAWR 67
Db 154 LSPDITTYEILAESSLG--YKNNTISAKDPLNSSTLFEFKYVNNVQRTFVWMD 211
OY 68 DLTSQDLRAITMLHTVESAFLADNLKTDIVRENTDNKLEVARLSTEGNLEDKF 127
Db 212 KLSVNHRRTHLTKLHMTVEQATLRISQFQTEFDNSTDIALKVFEPFSY-NMKIHP 270
OY 128 PENNGHSTIQLSANTLKONGRNGEIRVAFVNLNGLPY-SFENASMKGTALSTNHS 166
Db 271 HMMN-DGDYINIPPKRAAYDSNGNAVAFLYKSGISPLSSSDNPLKPDNDNSEEE 329
OY 187 VIVNSPYITAINKFEN--KVYLADPVFTVKHIKQSEENFNPCSFWSYKRTMGY 244
Db 330 RVISS-VISVMS--SNPFLVELEKITFTLSHRYT-DRYRSLCAFWMVSPDTMGSM 384
OY 245 STGCRLLTNKTHHTTSCNHLNFAVLA---HVEYKSDAVDLDLDVITWYGLISL 301
Db 385 SSECCELYTSENHTSCRNHLTHFAILMSSGSPSIGIKDYN-----ILTRITOLGIITSL 439
OY 302 VCLLICIFTCFPRGLQSDNRTIHKNCISLFEVALLFLGINFTDQPIACAVFAALLHF 361
Db 440 ICAICICFTFWFSEIOSTRTTIHKNCISLFEVALLFLGINFTDQPIACAVFAALLHF 499
OY 362 FFLAFTWMELEGVQYIMLVEFESESRKRYEYLVGYGMPALIVASAVDRSYGTD 421
Db 500 FFLAFAFMCMIEGHLHYVGVYVYKNGFLHKNFYIFGVLSPAVVGFSAALGRYGGT 559
OY 422 KVCMLRDTFIMSFIPALILMLNFIAGIALYKMFHTAILKPESGLDNIKSWVG 481
Db 560 KVCMLSTENNFIMSFIPALILMLNFIAGIALYKMFHTAILKPESGLDNIKSWVG 619
OY 482 AIALCLGLTMAFGLYNFIMSFIPALILMLNFIAGIALYKMFHTAILKPESGLDNIKSWVG 541
Db 620 AIALCLGLTMAFGLYNFIMSFIPALILMLNFIAGIALYKMFHTAILKPESGLDNIKSWVG 679
OY 542 R-THCCSG 548
Db 680 KNPCCCG 687

RESULT 3


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Query Match      23.9%; Score 1088.5; DB 10; Length 690;
Best Local Similarity 41.4%; Pred. No. 1.5e-77;
Matches 227; Conservative 111; Mismatches 189; Indels 21; Gaps 11;

QY 8 LMGADITYSVRANDQVLGLDVOLRNLTGPGKSAASLKKAWETVNNLLQPOLANMR 67
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DB 154 LSPDITTYEILAESSSLG--YKNNTISAKDTLSNSTLREPKVNNVQDRTEVYWD 211
   : : : : : : : : : : : : : : : : : : : : : : : : : : : :
QY 68 DLTSQDLRAATMLLTHVEESAFAVLADNLKTDIVRENTDNIKLEVARLSTEGNLEDLKF 127
   : : : : : : : : : : : : : : : : : : : : : : : : : : : :
DB 212 KLSVNNHRHTLTKLMTVEATLRISQSFOKTEFDNTSDIALKVFEPDSY-NMKIHP 270
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QY 128 PENMGHSTIQLSANLTKONGRGEIRAVFVLYNNLGPVL-STENASMKLGTALSTNHS 186
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DB 271 HMNN-DGDYINIPPKRAAVDSNGNVAFLYKKSIGPLSSSDNFLKPNYDNSEEE 329
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QY 187 VIYNSPVTIAIKFESN--KYVLADPVVTYVHKIKOSEENFNPNCSFMSYSKRTMGY 244
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DB 330 RVISS-VISVSMS--SNPPLYELEKITFTLSHRKYT-DRYSLCAFMYSPDTNMGSW 384
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QY 245 STQGCRLTLTNKTHHTSCNHLTNFAVLMA--HVEYKSHDAYHDLDDVITWYGLIISL 301
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DB 385 SSGCELTYSNETHHTSCRNHLTHFALMSSGSGSIGIKDYN-----ILTRITQIGIITSL 439
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QY 302 VCLLICITFCFFRGLOSDRNTIHKNLCLSLFVAELLFLGINRTDPIACAVFALLHF 361
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DB 440 ICLATCFEFPFSEIOSTRRTTIHKNLCSLFLAEVLGVINTMTNKLKCSITAGLHY 499
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QY 362 FFLAATYMMLEGVOLYIMLVEVFESHRSKRKFYLVGYGMPALIVASAVDYRSCTD 421
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DB 500 FFLAATFAAMCIEGIIHLYLVGVYNNKGFLLKMFYIFGVYSPAVVGFSAALGRYGGT 559
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QY 422 KVCMLRLDTYFMSFGPATLIIMLVIFGLIKMFMHTALIKPSSGCLDNKISVIG 481
   : : : : : : : : : : : : : : : : : : : : : : : : : : : :
DB 560 KVCMLSTENNFIISFGIPACIIIVNLACVILIKYFRITAGIKREVSFENIRSCARG 619
   : : : : : : : : : : : : : : : : : : : : : : : : : : : :
QY 482 AIALLCILGTYMAGLWYNESVIMAYLFTFNSLQGMFIIFHCYLQKRVREYKCL 541
   : : : : : : : : : : : : : : : : : : : : : : : : : : : :
DB 620 ALALFLGLTGTWIEGVLVHVASVYAVLYFTVSNAGFMFIFFLCVLSKRIGOEYRLF 679
   : : : : : : : : : : : : : : : : : : : : : : : : : : : :
QY 542 R-THCCSG 548
   : : : : : : : : : : : : : : : : : : : : : : : : : : : :
DB 680 KNPCCGFG 687
   : : : : : : : : : : : : : : : : : : : : : : : : : : : :

RESULT 5
US-09-909-088b-49
: Sequence 49, Application US/09909088B
: Patent No. US20020146709a1
: GENERAL INFORMATION:
: APPLICANT: Genentech, Inc.
: APPLICANT: Ashkenazi, Avi
: APPLICANT: Botstein, David
: APPLICANT: Desnoyers, Luc
: APPLICANT: Eaton, Dan L.
: APPLICANT: Ferrara, Napoleone
: APPLICANT: Filvaroff, Ellen
: APPLICANT: Fong, Sherman
: APPLICANT: Gao, Wei-Qiang
: APPLICANT: Gerber, Hanspeter
: APPLICANT: Gerltzen, Mary E.
: APPLICANT: Goddard, A.
: APPLICANT: Godowski, Paul J.
: APPLICANT: Grimaldi, Christopher J.
: APPLICANT: Gunney, Austin L.
: APPLICANT: Hillan, Kenneth, J.
: APPLICANT: Kljavin, Ivar J.
: APPLICANT: Mather, Jennie P.
: APPLICANT: Pan, James
: APPLICANT: Raoni, Nicholas F.
: APPLICANT: Roy, Margaret Ann
: APPLICANT: Stewart, Timothy A.
: APPLICANT: Tumas, Daniel

```

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APPLICANT: Williams, P. Mickey
APPLICANT: Wood, William, I.
TITLE OF INVENTION: Secreted and Transmembrane Polypeptides and Nucleic
TITLE OF INVENTION: Acids Encoding the Same
FILE REFERENCE: 10466-14
CURRENT APPLICATION NUMBER: US/09/909,088B
CURRENT FILING DATE: 2001-07-18
PRIOR APPLICATION NUMBER: PCT/US00/04414
PRIOR FILING DATE: 2000-02-22
PRIOR APPLICATION NUMBER: US 60/143,048
PRIOR FILING DATE: 1999-07-07
PRIOR APPLICATION NUMBER: US 60/145,698
PRIOR FILING DATE: 1999-07-26
PRIOR APPLICATION NUMBER: US 60/146,222
PRIOR FILING DATE: 1999-07-28
PRIOR APPLICATION NUMBER: PCT/US99/20594
PRIOR FILING DATE: 1999-09-08
PRIOR APPLICATION NUMBER: PCT/US99/20944
PRIOR FILING DATE: 1999-09-13
PRIOR APPLICATION NUMBER: PCT/US99/21090
PRIOR FILING DATE: 1999-09-15
PRIOR APPLICATION NUMBER: PCT/US99/21547
PRIOR FILING DATE: 1999-09-15
PRIOR APPLICATION NUMBER: PCT/US99/23089
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PRIOR APPLICATION NUMBER: PCT/US99/28214
PRIOR FILING DATE: 1999-11-29
PRIOR APPLICATION NUMBER: PCT/US99/28313
PRIOR FILING DATE: 1999-11-30
PRIOR APPLICATION NUMBER: PCT/US99/28564
PRIOR FILING DATE: 1999-12-02
PRIOR APPLICATION NUMBER: PCT/US99/28565
PRIOR FILING DATE: 1999-12-02
PRIOR APPLICATION NUMBER: PCT/US99/30095
PRIOR FILING DATE: 1999-12-16
PRIOR APPLICATION NUMBER: PCT/US99/30911
PRIOR FILING DATE: 1999-12-20
PRIOR APPLICATION NUMBER: PCT/US99/30999
PRIOR FILING DATE: 1999-12-20
PRIOR APPLICATION NUMBER: PCT/US00/00219
PRIOR FILING DATE: 2000-01-05
NUMBER OF SEQ ID NOS: 423
SEQ ID NO 49
LENGTH: 690
TYPE: PRT
ORGANISM: Homo sapiens
US-09-909-088b-49

Query Match      23.9%; Score 1088.5; DB 10; Length 690;
Best Local Similarity 41.4%; Pred. No. 1.5e-77;
Matches 227; Conservative 111; Mismatches 189; Indels 21; Gaps 11;

QY 8 LMGADITYSVRANDQVLGLDVOLRNLTGPGKSAASLKKAWETVNNLLQPOLANMR 67
   : : : : : : : : : : : : : : : : : : : : : : : : : : : :
DB 154 LSPDITTYEILAESSSLG--YKNNTISAKDTLSNSTLREPKVNNVQDRTEVYWD 211
   : : : : : : : : : : : : : : : : : : : : : : : : : : : :
QY 68 DLTSQDLRAATMLLTHVEESAFAVLADNLKTDIVRENTDNIKLEVARLSTEGNLEDLKF 127
   : : : : : : : : : : : : : : : : : : : : : : : : : : : :
DB 212 KLSVNNHRHTLTKLMTVEATLRISQSFOKTEFDNTSDIALKVFEPDSY-NMKIHP 270
   : : : : : : : : : : : : : : : : : : : : : : : : : : : :
QY 128 PENMGHSTIQLSANLTKONGRGEIRAVFVLYNNLGPVL-STENASMKLGTALSTNHS 186
   : : : : : : : : : : : : : : : : : : : : : : : : : : : :
DB 271 HMNN-DGDYINIPPKRAAVDSNGNVAFLYKKSIGPLSSSDNFLKPNYDNSEEE 329
   : : : : : : : : : : : : : : : : : : : : : : : : : : : :
QY 187 VIYNSPVTIAIKFESN--KYVLADPVVTYVHKIKOSEENFNPNCSFMSYSKRTMGY 244
   : : : : : : : : : : : : : : : : : : : : : : : : : : : :
DB 330 RVISS-VISVSMS--SNPPLYELEKITFTLSHRKYT-DRYSLCAFMYSPDTNMGSW 384
   : : : : : : : : : : : : : : : : : : : : : : : : : : : :
QY 245 STQGCRLTLTNKTHHTSCNHLTNFAVLMA--HVEYKSHDAYHDLDDVITWYGLIISL 301
   : : : : : : : : : : : : : : : : : : : : : : : : : : : :
DB 385 SSGCELTYSNETHHTSCRNHLTHFALMSSGSGSIGIKDYN-----ILTRITQIGIITSL 439
   : : : : : : : : : : : : : : : : : : : : : : : : : : : :
QY 302 VCLLICITFCFFRGLOSDRNTIHKNLCLSLFVAELLFLGINRTDPIACAVFALLHF 361
   : : : : : : : : : : : : : : : : : : : : : : : : : : : :

```

Db 440 ICALICITFWFSEIOSTRRTTIHKNLCCSLFLAELVFLVGINFTNKNLFCSTIINGLHY 499
Qy 362 FELAAFTWMELEGVOLYIMLVEVEFSEHSRRKRYFLVGYGMPALIVANSAADYRSGTD 421
Db 500 FELAAFTWMELEGVOLYIMLVEVEFSEHSRRKRYFLVGYGMPALIVANSAADYRSGTD 559
Qy 422 KVCWMLRDTYFWSFTIGPATLIMLVIFLGIALYKMFHHTAILEPESGCLDNIRKSWYG 481
Db 560 KVCWMLSTENNFTWSFTIGPATLIMLVIFLGIALYKMFHHTAILEPESGCLDNIRKSWYG 619
Qy 482 AIALICLIGTWPAGLMINVESTVIMAYLFTFNSLOGMFIFHCVLQKRYKREYRCL 541
Db 620 AIALICLIGTWPAGLMINVESTVIMAYLFTFNSLOGMFIFHCVLQKRYKREYRCL 679
Qy 542 R-THCCSG 548
Db 680 KNPCCFCG 687

RESULT 6

US-09-925-300-1407
Sequence 1407, Application US/09925300
Patent No. US20020151681A1
GENERAL INFORMATION:
APPLICANT: Craig Rosen,
APPLICANT: Steve Ruben,
TITLE OF INVENTION: Nucleic Acids, Proteins and Antibodies
FILE REFERENCE: PA101
CURRENT APPLICATION NUMBER: US/09/925,300
CURRENT FILING DATE: 2001-08-10
PRIOR APPLICATION NUMBER: PCT/US00/05988
PRIOR FILING DATE: 2000-03-08
PRIOR APPLICATION NUMBER: 60/124,270
PRIOR FILING DATE: 1999-03-12
NUMBER OF SEQ ID NOS: 1890
SOFTWARE: PatentIn ver. 2.0
SEQ ID NO 1407
LENGTH: 713
TYPE: PRT
ORGANISM: Homo sapiens
FEATURE:
NAME/KEY: SITE
LOCATION: (9)
OTHER INFORMATION: Xaa equals any of the naturally occurring L-amino acids
NAME/KEY: SITE
LOCATION: (10)
OTHER INFORMATION: Xaa equals any of the naturally occurring L-amino acids
NAME/KEY: SITE
LOCATION: (134)
OTHER INFORMATION: Xaa equals any of the naturally occurring L-amino acids
NAME/KEY: SITE
LOCATION: (280)
OTHER INFORMATION: Xaa equals any of the naturally occurring L-amino acids
NAME/KEY: SITE
LOCATION: (282)
OTHER INFORMATION: Xaa equals any of the naturally occurring L-amino acids
NAME/KEY: SITE
LOCATION: (322)
OTHER INFORMATION: Xaa equals any of the naturally occurring L-amino acids
US-09-925-300-1407

Query Match 23.9%; Score 1088.5; DB 10; Length 713;
Best Local Similarity 41.4%; Pred. No. 1.6e-77;

Matches 227; Conservative 109; Mismatches 191; Indels 21; Gaps 11;

Qy 8 LNAGDITVSAMDOLVGLDVLNLPKGSARSLNKAMVETVNNLLQPALNMR 67
Db 176 LSPDITVIELAESSLLG--YKNNITSAKDLISNSTLFEVYKTVANNFQROTFVYWD 233
Qy 68 DLTTSDOLRAATMLHVEESAFVLADNLKTDIVRENTDNKLEVARLSGNEIDKLF 127
Db 234 KLSVNHRTHTLKMHTVEQATLRLISQSFQKTFTEFDTNSTDIALKVK-FXDSYNKHIHP 292

Qy 128 PENMGSTIOASNTLKNONGEIRVAVLYNNIGPYL-STENASMKLSTEALSTNHS 186
Db 293 HMM--DGDVINFPKRAAYDSNGVAAVAFYTKSITGLISSDNFLKPOYDNDSEEE 351
Qy 187 VIVNSPVTAALNKEFSN--KVYADPVYFTVKIKOSEENPNPCSFWSYKRTMTGYW 244
Db 352 RVISS-VISVSMS---SNPPLYLELEKITFTLSHRKVT--DRYSLCAFWNYSPTDMNSW 406
Qy 245 STGCRLLTKTKTHTTCCSNHLTNFAVMA--HYEVKHSADVHLLDVTWVGLISL 301
Db 407 SSEGCLYFSMETHSCRNHLTHFAILMSGSPSIGIDYN----ILTRITOLGIIISL 461
Qy 302 VCLLCITFPCEPREGLOSRNTIHKNLCSLFLAELVFLVGINFTNKNLFCSTIINGLHY 361
Db 462 ICALICITFWFSEIOSTRRTTIHKNLCCSLFLAELVFLVGINFTNKNLFCSTIINGLHY 521
Qy 362 FELAAFTWMELEGVOLYIMLVEVEFSEHSRRKRYFLVGYGMPALIVANSAADYRSGTD 421
Db 522 FELAAFTWMELEGVOLYIMLVEVEFSEHSRRKRYFLVGYGMPALIVANSAADYRSGTD 581
Qy 422 KVCWMLRDTYFWSFTIGPATLIMLVIFLGIALYKMFHHTAILEPESGCLDNIRKSWYG 481
Db 582 KVCWMLSTENNFTWSFTIGPATLIMLVIFLGIALYKMFHHTAILEPESGCLDNIRKSWYG 641
Qy 482 AIALICLIGTWPAGLMINVESTVIMAYLFTFNSLOGMFIFHCVLQKRYKREYRCL 541
Db 642 AIALICLIGTWPAGLMINVESTVIMAYLFTFNSLOGMFIFHCVLQKRYKREYRCL 701
Qy 542 R-THCCSG 548
Db 702 KNPCCFCG 709

RESULT 7

US-09-978-486-5
Sequence 5, Application US/09978486
Patent No. US20020052015A1
GENERAL INFORMATION:
APPLICANT: Lin, Yi-Jyun
APPLICANT: Benzer, Seymour
TITLE OF INVENTION: METHODS OF USE
TITLE OF INVENTION: METHODS OF USE
FILE REFERENCE: 06618/343001
CURRENT APPLICATION NUMBER: US/09/978,486
CURRENT FILING DATE: 2001-10-15
PRIOR APPLICATION NUMBER: US/09/370,098
PRIOR FILING DATE: 1999-08-06
PRIOR APPLICATION NUMBER: 60/095,826
PRIOR FILING DATE: 1998-08-07
NUMBER OF SEQ ID NOS: 6
SOFTWARE: FastSeq for Windows Version 4.0
SEQ ID NO 5
LENGTH: 240
TYPE: PRT
ORGANISM: Rattus norvegicus
US-09-978-486-5

Query Match 20.3%; Score 927; DB 10; Length 240;
Best Local Similarity 67.5%; Pred. No. 1.6e-65;
Matches 162; Conservative 46; Mismatches 37; Indels 0; Gaps 0;

Qy 285 HDLIDVTWGIILSLVLCIGTFCPCFREGLOSRNTIHKNLCSLFLAELVFLGIN 344
Db 1 NELLISVITWGIIVISLCLACISFCFLRQIDRNTIHKNLCSLFLAELVFLVGIN 60
Qy 345 RPDQIACAVRALHFFFLAFTWMELEGVOLYIMLVEVEFSEHSRRKRYFLVGYGPA 404
Db 61 KTOYEVACPTRAGLHYFLAFLSWCLGVALYLLVLEVESESRKRYYLGGYCPA 120
Qy 405 LIVANSAVDYRSGTDVWMLRDTYFWSFTIGPATLIMLVIFLGIALYKMFHHTAI 464
Db 405 LIVANSAVDYRSGTDVWMLRDTYFWSFTIGPATLIMLVIFLGIALYKMFHHTAI 464

Db 121 LVVGIAAIDYNSYTEKACWLRVNFYIWSIFGVPVSEVIVNLVFLMTLHKMINSSV 180
Oy 465 LKRESCLDNIKSMVIGATALLCLGLTMAFGMYINVESTIVMAYFTTFNSLOGMEFI 524
Db 181 LKPDSSRLDNKIKSMALGATALLFLGLTMAFGMLFINKESVMAVYFTTFNAGQVFI 240

RESULT 8
US-09-764-853-679
; Sequence 679, Application US/09764853
; Patent No. US20020090672A1
; GENERAL INFORMATION:
; APPLICANT: Rosen et al.
; TITLE OF INVENTION: Nucleic Acids, Proteins, and Antibodies
; FILE REFERENCE: P1206
; CURRENT APPLICATION NUMBER: US/09/764,853
; CURRENT FILING DATE: 2001-01-17
; Prior application data removed - consult PALM or file wrapper
; NUMBER OF SEQ ID NOS: 939
; SOFTWARE: PatentIn Ver. 2.0
; SEQ ID NO 679
; LENGTH: 661
; TYPE: PRT
; ORGANISM: Homo sapiens
US-09-764-853-679

Query Match 17.0%; Score 776; DB 10; Length 661;
Best local Similarity 33.6%; Pred. No. 5,3e-53;
Matches 184; Conservative 102; Mismatches 229; Indels 32; Gaps 11;

Oy 35 TPGGKDSAAASLKNKAVEYVNNLLOPOLAMWDLTTSQDLRAATMLLHVEESAVLAD 94
Db 129 TTSSKTTGGKELQKIVDFESLITNQTLL--WRTEGROEISSTATTILLRDESKVLETAL 186
Oy 95 NLKTDIVRENTDNIRKLEVARLSTEGNLEDLKPENMGHSTIQLSANLTKQNGRGEIR 154
Db 187 KPEQVAVLKIQNSVAIEQAITDNCSEKRTFNLVNQMS--MDICSDIIGDGTGQPSA 245
Oy 155 VAEVLVNNIGPYLSTENASMKLSTENSHSVIVNSPVITAAINKESKRYLADPVVF 214
Db 246 IAFISYSLGNIIT--NAF--FEEMDKKDYVLNSQVSAIGRK--RNVSLSKSVTL 297
Oy 215 TVKHIOSEENFNPNCSFMSYSKRTMTG--YWSOGCRLLTNTKTHPTTSCNHLTNFAVLM 273
Db 298 TFOHVAKMTPESTKRVFCVYV--KSTGQGSQMSRDGCFLLHVNKSHTMCSHLSFAVLM 354
Oy 274 AHEVYHSDAVHDLDDVTIWMGILLSVCLLCITFEFCFRGLQSDRNTIHNLCISLF 333
Db 355 ALTSQE-----EDPVLVITVYGLSVSLCLLALFLCKAIONTSTSLHLQSLCLF 409
Oy 334 VAEFLFLIGINRTDPIACAVFPAALHFFFLAFTWMLFEGVOLYI---MLVEFESEH 389
Db 410 LAHLFLVIGIDRTERPVLCISIIGALHLYLAFLAFTWMLLEGVHLFLARNLTVVNSSIN 469
Oy 390 SRRKY--FYLVGMPALIVASAAVDYRSYGTDKVCMRLDTYFIWSIFGAPATLITMLNV 448
Db 470 RLKMWIMFPGYGVPAVTAISAASMPHLGYTADRCWHLHDGFMMSFLGPAIFSAANL 529
Oy 449 IFGLIALYKMFHHTAILKPESGCLDNKISVIGATIALALLCLGLTMAFGMYINVESTIVMA 508
Db 530 VLEFLVFWMLKRLSLNSVSTIQTNRMLAFATAQLFLGCTWGLQVPAQVMA 589
Oy 509 YLFTFINSLOGMFIETFHCVLQKKVREYKGLRTHCCSGKSTESSISGSK-----TS 561
Db 590 YLFTIINSLOGFFIFLYVCLLSQVQKQYOKWREIYKKSSEBETITLSSKMPDPSKPS 649
Oy 562 GSRTPGR 568
Db 650 GDVFPQ 656

RESULT 9
US-09-764-898-224

; Sequence 224, Application US/09764898
; Patent No. US20020090673A1
; GENERAL INFORMATION:
; APPLICANT: Rosen et al.
; TITLE OF INVENTION: Nucleic Acids, Proteins, and Antibodies
; FILE REFERENCE: P1201
; CURRENT APPLICATION NUMBER: US/09/764,898
; CURRENT FILING DATE: 2001-01-17
; Prior application data removed - consult PALM or file wrapper
; NUMBER OF SEQ ID NOS: 311
; SOFTWARE: PatentIn Ver. 2.0
; SEQ ID NO 224
; LENGTH: 661
; TYPE: PRT
; ORGANISM: Homo sapiens
US-09-764-898-224

Query Match 17.0%; Score 776; DB 10; Length 661;
Best local Similarity 33.6%; Pred. No. 5,3e-53;
Matches 184; Conservative 102; Mismatches 229; Indels 32; Gaps 11;

Oy 35 TPGGKDSAAASLKNKAVEYVNNLLOPOLAMWDLTTSQDLRAATMLLHVEESAVLAD 94
Db 129 TTSSKTTGGKELQKIVDFESLITNQTLL--WRTEGROEISSTATTILLRDESKVLETAL 186
Oy 95 NLKTDIVRENTDNIRKLEVARLSTEGNLEDLKPENMGHSTIQLSANLTKQNGRGEIR 154
Db 187 KPEQVAVLKIQNSVAIEQAITDNCSEKRTFNLVNQMS--MDICSDIIGDGTGQPSA 245
Oy 155 VAEVLVNNIGPYLSTENASMKLSTENSHSVIVNSPVITAAINKESKRYLADPVVF 214
Db 246 IAFISYSLGNIIT--NAF--FEEMDKKDYVLNSQVSAIGRK--RNVSLSKSVTL 297
Oy 215 TVKHIOSEENFNPNCSFMSYSKRTMTG--YWSOGCRLLTNTKTHPTTSCNHLTNFAVLM 273
Db 298 TFOHVAKMTPESTKRVFCVYV--KSTGQGSQMSRDGCFLLHVNKSHTMCSHLSFAVLM 354
Oy 274 AHEVYHSDAVHDLDDVTIWMGILLSVCLLCITFEFCFRGLQSDRNTIHNLCISLF 333
Db 355 ALTSQE-----EDPVLVITVYGLSVSLCLLALFLCKAIONTSTSLHLQSLCLF 409
Oy 334 VAEFLFLIGINRTDPIACAVFPAALHFFFLAFTWMLFEGVOLYI---MLVEFESEH 389
Db 410 LAHLFLVIGIDRTERPVLCISIIGALHLYLAFLAFTWMLLEGVHLFLARNLTVVNSSIN 469
Oy 390 SRRKY--FYLVGMPALIVASAAVDYRSYGTDKVCMRLDTYFIWSIFGAPATLITMLNV 448
Db 470 RLKMWIMFPGYGVPAVTAISAASMPHLGYTADRCWHLHDGFMMSFLGPAIFSAANL 529
Oy 449 IFGLIALYKMFHHTAILKPESGCLDNKISVIGATIALALLCLGLTMAFGMYINVESTIVMA 508
Db 530 VLEFLVFWMLKRLSLNSVSTIQTNRMLAFATAQLFLGCTWGLQVPAQVMA 589
Oy 509 YLFTFINSLOGMFIETFHCVLQKKVREYKGLRTHCCSGKSTESSISGSK-----TS 561
Db 590 YLFTIINSLOGFFIFLYVCLLSQVQKQYOKWREIYKKSSEBETITLSSKMPDPSKPS 649
Oy 562 GSRTPGR 568
Db 650 GDVFPQ 656

RESULT 10
US-09-992-647-1
; Sequence 1, Application US/09992647
; Patent No. US20020146787A1
; GENERAL INFORMATION:
; APPLICANT: Xu, Hong
; APPLICANT: Coahan, Victoria L.
; APPLICANT: Stuart, Susan G.
; TITLE OF INVENTION: HUMAN EMRI-LIKE G PROTEIN-COUPLED RECEPTOR
; FILE REFERENCE: PC-0052 CIP
; CURRENT APPLICATION NUMBER: US/09/992,647

```

; CURRENT FILING DATE: 2002-11-13
; NUMBER OF SEQ ID NOS: 12
; SOFTWARE: PERL Program
; SEQ ID NO 1
; LENGTH: 652
; TYPE: PRT
; ORGANISM: Homo sapiens
; FEATURE:
; NAME/KEY: misc.feature
; OTHER INFORMATION: Incyte ID No. US20020146767A1 429905
US-09-992-647-1

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```

Query Match          17.0%; Score 774; DB 10; Length 652;
Best Local Similarity 33.6%; Pred. No. 7,4e-53;
Matches 184; Conservative 102; Mismatches 229; Indels 32; Gaps 11;

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OY 35 TPGGDSARSINKAMVETVNNLQPOLANMRDLTTSQDLRAATMLLHTVESAEVLAD 94
D 120 TTSSKTQGRKELQKIVKFEESLITNQLT-WRTEGRQISSTATTILRDVESKYLETAL 177
OY 95 NLKTDIVRENTDNKLEVARLSTEGNLEDLKEPEMNGSGTQLSANTLKGNGRGEIR 154
D 178 KDPECKVLKIDMSVAIEQAITDNCSERKTFNLVQNN--MDIRCSDIQDTPQPSV 236
OY 155 VAFVLNNLGPYLSTENASMKLGTEALSTNHSVIVNSPYITAIKNEFSGNKYLAADPYVE 214
D 237 IAFIYSLSGNI---NMTF---FEEMDKKDOYLVNSQVSAIGPK--RNVSLSKSVTL 288
OY 215 TVKHAKOSEENFNPCSEFWSYSKRTMTG-YWSTQGRLLTTNKTHTTCSNHLTNFAVLM 273
D 289 TFOHKMPTSTKRVCCVW---KSTGQSGQMSRDCFLIHVNSKSHMCNCSHLSFAVLM 345
OY 274 AHVEKHSQAVHDDLDTVTWYGILSLVCLLICITFEFFFGLOSDRNTIHKNICISLF 333
D 346 ALTSGE-----EDPVLYITTYGSLVSLLCLLALFTFLCAIDONTSTSLHLQSLCLF 400
OY 334 VAEELFLIGINFTDPIACAVFAALLHFEFLAFTMPEEGVOLYI---MLVEVESEB 389
D 401 LAHLFLVIGIDTREPKEVCSITAGALHYTLAFTMMLLEGVHFLPTANLNVVNSTIN 460
OY 330 SRRKTFILVGYGMPALVYASAAVDYRSYGTDKVCWRLDTFTYFWSFGPATLITIMLV 448
D 461 RLKMKIMRPVGYAVVYVAISAASMPHLYGTADRCMLHLDQGFMSFGLPCALFSAVL 520
OY 449 IELGALYKMFHTALILRPESGCLDNKSWVIGAITALLCLLGLTNAFGMLINSEVIVA 508
D 521 VLFILVETMLKRLSSLSNSEVSTIONTRMLAFKATRAQLFLICCTWCLGLLQVPAQVNA 580
OY 509 YLETFINSLOGMEFIFHCVLQKRYRKEYGKCLRTHCCSGKSTESSIGSGK-----TS 561
D 581 YLETFINSLOGMEFIFHCVLQKRYRKEYGKCLRTHCCSGKSTESSIGSGK-----TS 561
OY 562 GSRTPGR 568
D 641 GDFPQGO 647

```

```

RESULT 11
US-09-992-647-11
; Sequence 11, Application US/09992647
; Patent No. US20020146767A1
; GENERAL INFORMATION:
; APPLICANT: Xu, Hong
; APPLICANT: Cohan, Victoria L.
; APPLICANT: Stuart, Susan G.
; TITLE OF INVENTION: HUMAN EMRI-LIKE G PROTEIN-COUPLED RECEPTOR
; FILE REFERENCE: PC-0052 CIP
; CURRENT APPLICATION NUMBER: US/09/992,647
; CURRENT FILING DATE: 2002-11-13
; NUMBER OF SEQ ID NOS: 12
; SOFTWARE: PERL Program
; SEQ ID NO 11
; LENGTH: 886

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; TYPE: PRT
; ORGANISM: Homo sapiens
; PUBLICATION INFORMATION:
; DATABASE ACCESSION NUMBER: Genbank ID No. US20020146767A1 9784994
US-09-992-647-11

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```

Query Match          15.7%; Score 715.5; DB 10; Length 886;
Best Local Similarity 30.4%; Pred. No. 4,6e-48;
Matches 166; Conservative 116; Mismatches 211; Indels 53; Gaps 12;

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OY 47 NKAMVETVNNLQPOLANMRDLTTSQDLRAATMLLHTVESAEVLAD-----NL 97
D 366 NKTTVVSLKNTSEFVPLVKQISMWTKFEETSLATVLESVE--SWTIASFMSAN 423
OY 98 KTDIVRENTDNKLEVARLSTEGNLEDLKEPEMNGSGTQLSANTLKGNGRGEIRVAF 157
D 424 VTPAVR--AEYLDIESKVINKECSEENVTL-DLVAGDMKIKICSCVIESESESTETTVAF 480
OY 158 VLYNNLGPYLSTENASMKLGTEALSTNHSVIVNSPYITAIKNEFSGNKY----- 207
D 481 VSEVGMESVLN-----ERFQDH-----QAPLTSEIKLKMNSRYVGGIMTECKD 526
OY 208 -LADPVVFTVKHAKOSEENFNPCSEFWSYSKRTMTGYWSTQGRLLTTNKTHTTCSNHL 266
D 527 GFSDDPIITYLENVQPKQFERPICVSGMSTDVK--GGWMTSPGCVILEASETYTICSCNQ 584
OY 267 TTFAYLMAHVEVKHSDAVHDDLDTVTWYGILSLVCLLICITFEFFFGLOSDRNTIHK 326
D 585 ANLAVTMASGEL---TYDFFSLYIISHVGIIISLCLVALATLFLCSIRHNHTYHL 639
OY 327 NLCISLVELLEFLIGINFTDPIACAVFAALLHFEFLAFTMPEEGVOLYIM-----L 381
D 640 HLCVCLLAKTLPLAGIRHKTDNKGCAITAGFHLFLACFMMLVEAVIPLFMANLKV 699
OY 382 VEVESEHSRRKYFYLVGYGMPALVYASAAVDYRSYGTDKVCWRLDTFTYFWSFGPAT 441
D 700 VNFESSRNKIMHLICAFGLPMLVVISASVQPGYGMHNRCLMTERGFIWSPGVC 759
OY 442 LILMLNVITLGLALYKMFHTALILRPESGCLDNKIKSWVIGAITALLCLLGLTNAFGML 501
D 760 TVIVINSLTLTWMLTILRORLSSVNAVESTLKDTRLTFKFAQAQLFLICCSWVLGIFQIG 819
OY 502 ESTVIMAYLETFINSLOGMEFIFHCVLQKRYRKEYGKCL--RTHCCSGKSTESSIGSGK 559
D 820 PVAQWAVLYLETFINSLOGAFIPLHCLLNGQVREYKRNITGTKRSQSQISRIILSSM 879
OY 560 TSGSRT 565
D 880 PSASKT 885

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RESULT 12
US-09-737-149-25
; Sequence 25, Application US/09737149
; Patent No. US20020077466A1
; GENERAL INFORMATION:
; APPLICANT: Spaderna, Steven K
; APPLICANT: Quinn, Kerry E.
; APPLICANT: Shinkels, Richard A.
; APPLICANT: Muralidhara, Padigaru
; APPLICANT: Spylek, Kimberly A.
; TITLE OF INVENTION: Polypeptides and Nucleic Acids Encoding Same
; FILE REFERENCE: 15966-620 CIP
; CURRENT APPLICATION NUMBER: US/09/737,149
; CURRENT FILING DATE: 2001-06-15
; PRIOR APPLICATION NUMBER: 60/170,564
; PRIOR FILING DATE: 1999-12-14
; PRIOR APPLICATION NUMBER: 60/173,165
; PRIOR FILING DATE: 1999-12-27
; PRIOR APPLICATION NUMBER: 60/173,362
; PRIOR FILING DATE: 1999-12-27
; PRIOR APPLICATION NUMBER: 60/173,544
; PRIOR FILING DATE: 1999-12-29

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: PRIOR APPLICATION NUMBER: 60/174,404
: PRIOR FILING DATE: 2000-01-04
: PRIOR APPLICATION NUMBER: 60/174,962
: PRIOR FILING DATE: 2000-01-07
: PRIOR APPLICATION NUMBER: 60/223,929
: PRIOR FILING DATE: 2000-08-09
: NUMBER OF SEQ ID NOS: 49
: SOFTWARE: Patentin Ver. 2.0
: SEQ ID NO 25
: LENGTH: 3034
: TYPE: PRT
: ORGANISM: Mus musculus
: US-09-737-149-25

```

Query Match	15.4%	Score 700.5	DB 10	Length 3034
Best Local Similarity	24.5%	Pred. No. 4,4e-46		
Matches 237	Conservative 166	Mismatches 356	Indels 207	Gaps 34

QY	1	AEONTNHLNADITY- -SVRAMDQVLGLDLOLRNLTGCGKQSAARSLN- -KAMETVKN	56
Db	2150	AKALRNATQGSSTLFGNDVRAAYOYLLAN- -LOHERQCGFDLAARFANFHDVYHTGSA	2208
QY	57	LLQPOLAMNRDLTTSQDLRAATMLH- ------TVEBSAFVLADNLKTDI	101
Db	2209	LLAPRTEASMEQIORS- -EAGAQAOLLRHEAFESNVARNVKRTYLRPFVLTNMTLAVDI	2267
QY	102	VRE- ------NNDNIKLEVAR- -LSTEGLEDLCKPREMNGHSTIOL- -	139
Db	2268	FDKLNFTGAQVPREDIDOELEPRELESSSPFADFFKPREK- -EBSVVRLTNRRTPLTA	2326
QY	140	-----SANTLKONGRNGELTRVAF- -VYNNMIGPL- -STENASMKLTGALST	183
Db	2327	QPREPARETSSSRRRRRRDERGQCAVALVYIRTLGQLLRPHYDRHNSLPLRNP- -	2383
QY	184	NHSVYNSPVITTAINKESKNVYADRVYFVKIKITQSEENFNPNCSSWYSKRT- -MTG	242
Db	2384	-----VINPVYVSAMVYSGTLPSPSLQRPRIWEFSILETEERKSRYCVFMNHSIDLTGGG	2439
QY	243	YMSPOGCRLLTYNKNHTCTSCNHLNPFVILMAHVEUKSDAVIDLDITVWVGLTSLV	302
Db	2440	GMSAKGCELLSRNKHVYQCSHSSCAVLNDSIKREGEV- -LPKITYTALSLSLV	2496
QY	303	CLLICITFFCFEFGRIQSDRNTIHKNLCTSLVEAEILLTIGINTROPICAVAFALHFE	362
Db	2497	ALLVAFVLLSEVRLTSLNLSHMKMLALAFESQILFMVGINQGTENPFLCTVVALILHY	2556
QY	363	FLAFTWMEFEGUOYLIMLVEFESEHNRKRFYLVGCMRALIYAVSAANDVYRSGTDK	422
Db	2557	SMGTAAMLVLELHLYRMLTEVRNIDGTGMRVHVGWGPRAIVGLAAGLDPOGGND	2616
QY	423	VCWLRLDYFPIWMSFGPRTLITMLN- -VIFL- -GIALKMFHNTAILKRESGLDNIKSM	478
Db	2617	FCWLSDOOLTLWSPFGRPGVYIIINTVYFVLBSAKVSCQKRNHY- -YERKGVNSMLRT-	2671
QY	479	VIGAIALLCLGLTWAFBLMYINESTVIMAYULEFTFNSIQGMEFIFHCVLQKKVRYEX-	537
Db	2672	--AFLLILLVATWLLDLAVNSOTLSEFHYFEAFPSQCIJFVLLFHCVARREYRKHJR	2728
QY	538	-----GKCLRTHCQSGKSPRESSIGSKTSGSRPGVYSGSOSGIRRMNDVYRKQSESEF	593
Db	2729	AVLACKKIQLD- -DSATTRATLTLRSLCQNN- -YSEBP- ------DMJR- -	2767
QY	594	ITGDINSASINREGILNARDTSV- ----MDPLPLNGHNGNSYASIGEYLSNCVOIIDR	649
Db	2768	-TALGESYASLD- ----STTRREGVQKLSYSSGPARGNHGERDT- ----SFIRNSMK	2814
QY	650	GYNNHETALEKKILKELTSNTYPSYLNHNHSSSEONRLMN- ------KLVNVL	696
Db	2815	AHGPRSDSDSELSIDHESSSYAASHTSDSEDDGGAEDKMNPAAGCAPHSTPKADALAHV	2874
QY	697	GGSGRDDAIVLDDATSFNHEESLIGEL- ----IHE- ------ESAPILPRV	737
Db	2875	PAGWPDESACSDSELDTEPHLKVETVYVELHQAQGNHCGDRSPDESSVLAKPAV	2934

```

Oy  738  xSTENHQPHNHTRRIRPOHSESEF-----PLLT--NEHNEEDLOSPIROSLY  782
Db  2935  LSSO-----POEGRGILNKNYTPPEPLPEOPLSKRLRLKLADCSQSTSSRT  2982
Oy  783  TSMPTLAGVATESVT--STOREPPAKGDAEDVYKSMENLGRNHVHOLHTYVOLD  840
Db  2983  SSSLGSGGVANHTDVTITIKTPREP-----GREHLNVAMNVATG  3022
Oy  841  RGSSDG  846
Db  3023  SAQANG  3028

```

RESULT 13
 US-09-737-149-30
 : Sequence 30. Application US/09737149
 : Patent No. US20020077466A1
 :
 : GENERAL INFORMATION:
 :
 : APPLICANT: Spaderna, Steven K
 : APPLICANT: Quinn, Kerry E.
 : APPLICANT: Shinkets, Richard A.
 : APPLICANT: Muralidhara, Padigaru
 : APPLICANT: Soytek, Kimberly A.
 :
 : TITLE OF INVENTION: Polypeptides and Nucleic Acids Encoding Same
 :
 : FILE REFERENCE: 15966-620 CIP
 :
 : CURRENT APPLICATION NUMBER: US/09/737,149
 :
 : PRIOR FILING DATE: 2001-06-15
 :
 : PRIOR APPLICATION NUMBER: 60/170,564
 :
 : PRIOR FILING DATE: 1999-12-14
 :
 : PRIOR APPLICATION NUMBER: 60/173,165
 :
 : PRIOR FILING DATE: 1999-12-27
 :
 : PRIOR APPLICATION NUMBER: 60/173,362
 :
 : PRIOR FILING DATE: 1999-12-27
 :
 : PRIOR APPLICATION NUMBER: 60/173,544
 :
 : PRIOR FILING DATE: 1999-12-29
 :
 : PRIOR APPLICATION NUMBER: 60/174,404
 :
 : PRIOR FILING DATE: 2000-01-04
 :
 : PRIOR APPLICATION NUMBER: 60/174,962
 :
 : PRIOR FILING DATE: 2000-01-07
 :
 : PRIOR APPLICATION NUMBER: 60/223,929
 :
 : PRIOR FILING DATE: 2000-08-09
 :
 : NUMBER OF SEQ ID NOS: 49
 :
 : SOFTWARE: PatentIn Ver. 2.0
 :
 : SEQ ID NO 30
 :
 : LENGTH: 3034
 :
 : TYPE: PRT
 :
 : ORGANISM: Mus musculus
 :
 : US-09-737-149-30

Query Match	15.48;	Score 700.5;	DB 10;	Length 3034;
Best Local Similarity	24.58;	Pred. No. 4.4e-46;		
Matches 237;	Conservative 166;	Mismatches 356;	Indels 207;	Gaps

```

Oy      1 AEOGRNHLNMGDITY--SVAMQOVLGILDVQORNTPTGKDSAAKSLC--KAMEYVNN 56
         | | | | | | | | | | | | | | | | | | | | | | | | | | | |
Db      2150 AKALRNATQGNSTLFGNDVYTAQQLART-LQHSNQSGFDLAATREANFEDVYHTSSA 2208
         | | | | | | | | | | | | | | | | | | | | | | | | | | | |
Oy      57 LLOQALNAMBDLTTSQDLRAATMLH-----TWESAFVLADNLKTDI 101
         | | | | | | | | | | | | | | | | | | | | | | | | | | | |
Db      2209 LLAPEATESWEOIORS-EAQAADLLRHFAYESNNVARNKRTYLPRPVLTANMLTAVDI 2267
         | | | | | | | | | | | | | | | | | | | | | | | | | | | |
Oy      102 VRE-----MNDNKLKELVAR--LSTEGNLEOLKPPENNGHSTQL----- 139
         | | | | | | | | | | | | | | | | | | | | | | | | | | | |
Db      2268 FDKLNTGGAOVPRFEDIQEELPRELESSVSPFADTFKPRPEK-BGRVVALTRRRTPLTA 2326
         | | | | | | | | | | | | | | | | | | | | | | | | | | | |
Oy      140 -----SANTLKQNGRNGEIRYAF-VLYNMLGPLY-----STENASMKLGTEALST 183
         | | | | | | | | | | | | | | | | | | | | | | | | | | | |
Db      2327 QPERRAERETSSSRRRNPRDEPQAFVALVIRTLGQLLRPHYDRHSLRLPRP--- 2383
         | | | | | | | | | | | | | | | | | | | | | | | | | | | |
Oy      184 NHSIVTSPVITAIANKFENSKUYLADRVVFTYKHKILOSEENFNQNCSPWSYSKRT-MTG 242
         | | | | | | | | | | | | | | | | | | | | | | | | | | | |
Db      2384 ---VINTPVASAVNYSEGPRPSSIQRLPIVFEESLTFEESKRCVCFWMNLSLDTGSG 2439
         | | | | | | | | | | | | | | | | | | | | | | | | | | | |

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Tue Dec 10 13:27:10 2002

us-09-744-226a-1.rapb

Page 10

[illegible]

```

RESULT 15
US-09-808-571A-2
: Sequence 2, Application US/09808571A
: Patent No. US20020106723A1
: GENERAL INFORMATION:
: APPLICANT: Bayer Aktiengesellschaft
: TITLE OF INVENTION: Receptor for latrotoxin from insects
: FILE REFERENCE: Le A 34 402
: CURRENT APPLICATION NUMBER: US/09/808, 571A
: CURRENT FILING DATE: 2000-03-14
: PRIOR APPLICATION NUMBER: DE 100 13 580.3
: PRIOR FILING DATE: 2000-03-18
: NUMBER OF SEQ ID NOS: 6
: SOFTWARE: PatentIn Ver. 2.1
: SEQ ID NO 2
: LENGTH: 1447
: TYPE: PRP
: ORGANISM: Drosophila melanogaster
: US-09-808-571A-2

```

Query Match	14.7%	Score 670.5;	DB 10;	Length 1447;
Best Local Similarity	29.2%	Pred. No. 3.3e-44;		
Matches 186;	Conservative 121;	Mismatches 268;	Indels 63;	Gaps 20

```

QY 39 KDSARFINKAMETVYNNLLPOALNAMRLTJTDQRAATMLHTVESAPALDNLLK 98
   :: :: :: :: :: :: :: :: :: :: :: :: :: :: :: :: :: :: :: ::
Db 508 REAMIMELLCVYKTSGNLDESOSSMIDLNPEDOMKATSLTGLGLENAPLADDTIIR 567
   :: :: :: :: :: :: :: :: :: :: :: :: :: :: :: :: :: :: :: ::
QY 99 TDIVRENTDNKLEVARLSTEGNLEDLKPPENNG--HGSTQLSANLTKONGREAIRV 155
   :: :: :: :: :: :: :: :: :: :: :: :: :: :: :: :: :: :: :: ::
Db 568 ERSVQKVRKNILLSVRLKTEKTIOSSVPPDPDQWPLSDRIETLPRALINDSEGLVRI 627
   :: :: :: :: :: :: :: :: :: :: :: :: :: :: :: :: :: :: :: ::
QY 156 AFVYNNLNGYLL--STFNASMKLG--SEALSTNHS-----VYNSPITAIKKE 201
   :: :: :: :: :: :: :: :: :: :: :: :: :: :: :: :: :: :: :: ::
Db 628 VFAAFDLESILKPSYDHPKSSRSYALISLDSVDNAGEIDQRLIRLMSKYTSLGK- 686
   :: :: :: :: :: :: :: :: :: :: :: :: :: :: :: :: :: :: :: ::
QY 202 FSKRVYLADPVFVTKHIKOSSEENPNPNSFWSYKRTMTGYWSTOGCRLLTNTKTHTTC 261
   :: :: :: :: :: :: :: :: :: :: :: :: :: :: :: :: :: :: :: ::
Db 687 -GRHIQLOSPITTLTKLKLK-TENVTPQCFVWNYIDHA---WSANGCSLESTNTHSVC 740
   :: :: :: :: :: :: :: :: :: :: :: :: :: :: :: :: :: :: :: ::
QY 262 SCHNLTNEAVLMAHV--EVKHS--DAVNDLLDVTYWGILLSVCLLTCFECFCFRG--L 317
   :: :: :: :: :: :: :: :: :: :: :: :: :: :: :: :: :: :: :: ::
Db 741 SCHNLTNEALMDVDEHQSLFTMPDGNKRIFTYISICICVVFYIALTLTKLENGYFV 800
   :: :: :: :: :: :: :: :: :: :: :: :: :: :: :: :: :: :: :: ::
QY 318 QSDRNTIHNKNCISLPAVELLLIGINRTDQPIACAVFALLHFFFLAFTMPLGVOYL 377
   :: :: :: :: :: :: :: :: :: :: :: :: :: :: :: :: :: :: :: ::
Db 801 KSARTSIYTSIYCLLALIEFLFGLTEGETSIFEGCFITFLPHCALISSTAMFCYEAFHS 860
   :: :: :: :: :: :: :: :: :: :: :: :: :: :: :: :: :: :: :: ::
QY 378 YI-----MLVEVESEHSRKRKFEYVCGMPALLVAAVAANDVSYSGDKYCWL-RDVT 430
   :: :: :: :: :: :: :: :: :: :: :: :: :: :: :: :: :: :: :: ::
Db 861 YSTISDEBLEV--DQTPKVNCTYILSTGLSISVAISLVLDIPSTYONDVCVMEANA 918
   :: :: :: :: :: :: :: :: :: :: :: :: :: :: :: :: :: :: :: ::
QY 431 YFIMSFIGPATL--IIMLVNIFGLIALYNNFHHTALIKESGOLDNISKWYIGAITALLCL 488
   :: :: :: :: :: :: :: :: :: :: :: :: :: :: :: :: :: :: :: ::
Db 919 LEYATFVYIPALVEFVAALIGTFELSMIMCRKSRPTGLKTEHRTLASVREDINCSPVILL 978
   :: :: :: :: :: :: :: :: :: :: :: :: :: :: :: :: :: :: :: ::
QY 489 LGLTMAGLMYI-----NSSTIYMAVLFPIRNSLOGMFIIFRVCYLAKKVAKEGCKLR 542
   :: :: :: :: :: :: :: :: :: :: :: :: :: :: :: :: :: :: :: ::
Db 979 LSAVWCASFYLLGAKMDQTDADVCEYCFCEFTLLGLVIFEHCHQNKIRREKRVYR 1038
   :: :: :: :: :: :: :: :: :: :: :: :: :: :: :: :: :: :: :: ::

```

```

OY 543 THC-----CGSGTSSST--CGSGTSGRPRGRSTSSOSRI-----RRMMNDTVKRO 588
      |         |         |         |         |         |         |         |
Db 1039 OHAWLPKCLKCKSKTSISSGIVTGNQPTAG--TLCSTYSTCKRKLPLGVSSEAHDDPQQDQ 1096
      |         |         |         |         |         |         |         |
OY 589 SESEFTTGDIINSSALNREGLLNMNADTVSMPLPLNG 626
      |         |         |         |         |         |         |         |
Db 1097 QTPVPTIEDAIMGATSDCE--LNEAQQORTLSSGLMTG 1132
      |         |         |         |         |         |         |         |

```

Search completed: December 10, 2002, 11:13:51
Job time : 27 secs

Sequences producing significant alignments:

(bits) Value

gi 3882257 dbj BAA34488.1	KIAA0768 protein [Homo sapiens]	203	3e-52	L
gi 14149677 ref NP_056051.1	lectomedin-3 [Homo sapiens] >g...	202	5e-52	L
gi 7513950 pir T17199	CL3BB protein - rat >gi 3695143 gb A...	199	6e-51	
gi 7513509 pir T18398	latrophilin-3, splice variant bbag, ...	199	8e-51	
gi 7513512 pir T18408	latrophilin-3, splice variant bbbg, ...	199	8e-51	
gi 7513951 pir T17200	CL3BC protein - rat >gi 3695145 gb A...	198	1e-50	
gi 7513510 pir T18405	latrophilin-3, splice variant bbah, ...	198	1e-50	
gi 7513513 pir T18409	latrophilin-3, splice variant bbbh, ...	198	1e-50	
gi 7513947 pir T17187	CL3AB protein - rat >gi 3695137 gb A...	198	1e-50	
gi 7513506 pir T18393	latrophilin-3, splice variant abbg, ...	197	2e-50	
gi 7513503 pir T18390	latrophilin-3, splice variant abag, ...	197	2e-50	
gi 7513948 pir T17188	CL3AC protein - rat >gi 3695139 gb A...	197	2e-50	
gi 7513504 pir T18391	latrophilin-3, splice variant abah, ...	197	2e-50	
gi 7513507 pir T18394	latrophilin-3, splice variant abbh, ...	197	2e-50	
gi 18677755 ref NP_570835.1	calcium-independent alpha-latrophilin...	196	4e-50	L
gi 7513949 pir T17198	CL3BA protein - rat >gi 3695141 gb A...	196	6e-50	
gi 7513508 pir T18395	latrophilin-3, splice variant bbaf, ...	195	9e-50	
gi 7513511 pir T18407	latrophilin-3, splice variant bbbf, ...	195	1e-49	
gi 7513946 pir T17186	CL3AA protein - rat >gi 3695135 gb A...	194	1e-49	
gi 7513502 pir T18389	latrophilin-3, splice variant abaf, ...	194	2e-49	
gi 7513505 pir T18392	latrophilin-3, splice variant abbf, ...	194	2e-49	
gi 7021080 dbj BAA91375.1	unnamed protein product [Homo sa...]	150	2e-36	
gi 5880492 gb AAD54676.1 AF104938.1	lectomedin-1 beta [Homo...]	114	2e-25	L
gi 5880490 gb AAD54675.1 AF104266.1	lectomedin-1 alpha [Hom...]	114	2e-25	L
gi 6912464 ref NP_036434.1	latrophilin 1; KIAA0786 protein...	114	3e-25	L
gi 7513501 pir T18383	latrophilin-2, splice variant bbabe ...	112	8e-25	
gi 7513491 pir T18381	latrophilin-2 (splice variant bbaae)...	112	8e-25	
gi 7513498 pir T18301	latrophilin-2, splice variant baaae ...	112	9e-25	
gi 7513500 pir T18367	latrophilin-2, splice variant baabe ...	112	9e-25	
gi 7513492 pir T18382	latrophilin-2 (splice variant bbaaf)...	112	1e-24	
gi 7513493 pir T18384	latrophilin-2 (splice variant bbabf)...	112	1e-24	
gi 7513486 pir T18370	latrophilin-2 (splice variant baabf)...	112	1e-24	
gi 7513499 pir T18366	latrophilin-2, splice variant baaaf ...	112	1e-24	
gi 7513941 pir T17157	CL2AA protein - rat >gi 3695123 gb A...	106	6e-23	
gi 11280659 pir T46611	CL2BB protein - rat >gi 3695131 gb ...	106	6e-23	
gi 7513942 pir T17158	CL2AB protein - rat >gi 3695125 gb A...	106	6e-23	
gi 7513944 pir T17160	CL2BA protein - rat >gi 3695129 gb A...	106	6e-23	
gi 7513943 pir T17159	CL2AC protein - rat >gi 3695127 gb A...	106	6e-23	
gi 19705539 ref NP_599235.1	calcium-independent alpha-latrophilin...	106	7e-23	L
gi 7513945 pir T17185	CL2BC protein - rat >gi 3695133 gb A...	106	7e-23	
gi 3882293 dbj BAA34506.1	KIAA0786 protein [Homo sapiens]	103	4e-22	L
gi 7513494 pir T18385	latrophilin-2 (splice variant bbbae)...	103	5e-22	
gi 7513496 pir T18387	latrophilin-2 (splice variant bbbbe)...	103	5e-22	
gi 7513487 pir T18375	latrophilin-2 (splice variant babae)...	103	5e-22	
gi 7513489 pir T18379	latrophilin-2 (splice variant babbe)...	103	6e-22	
gi 7513495 pir T18386	latrophilin-2 (splice variant bbbaf)...	103	6e-22	
gi 7513497 pir T18388	latrophilin-2 (splice variant bbbbf)...	103	6e-22	
gi 7513488 pir T18377	latrophilin-2 (splice variant babaf)...	103	6e-22	
gi 7513490 pir T18380	latrophilin-2 (splice variant babbf)...	103	6e-22	
gi 7513938 pir T17145	CL1AB protein - rat >gi 3695117 gb A...	86	8e-17	
gi 7513940 pir T17156	CL1BB protein - rat >gi 3695121 gb A...	86	8e-17	
gi 12621148 ref NP_075251.1	CL1BA protein [Rattus norvegic...]	86	1e-16	L
gi 7513937 pir T17138	CL1AA protein - rat >gi 2213659 gb A...	86	1e-16	
gi 7662324 ref NP_055736.1	lectomedin-2; KIAA0821 protein ...	85	2e-16	L
gi 11037014 gb AAG27461.1 AF307079.1	lectomedin-2 [Homo sap...]	85	2e-16	L
gi 7513485 pir T18413	latrophilin-1, brain-specific - bovi...	84	4e-16	
gi 7513484 pir T18411	latrophilin-1, brain-specific - bovi...	84	4e-16	
gi 14043198 gb AAH07587.1 AAH07587	Unknown (protein for IMA...)	50	4e-06	L
gi 21301476 gb EAA13621.1	agCP7645 [Anopheles gambiae str....]	44	3e-04	
gi 22024081 ref NP_610397.2	CG8639 gene product [Drosophil...]	43	8e-04	L
gi 11545908 ref NP_071442.1	EGF-TM7-latrophilin-related pr...	38	0.020	L

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gi 15806511 ref NP_295222.1 	NADH dehydrogenase I, G subuni...	<u>33</u>	0.81	
gi 18875378 ref NP_573485.1 	ETL1 [Mus musculus] > gi 144233...	<u>30</u>	8.0	L

Alignments

Get selected sequences

Select all

Deselect all

☐ >[gi|3882257|dbj|BAA34488.1|](#) KIAA0768 protein [Homo sapiens]
Length = 872

Score = 203 bits (517), Expect = 3e-52
Identities = 105/120 (87%), Positives = 105/120 (87%)

Query: 1 AENTRNHLNAGDITYSVRAMDNLVGLLDVNLRLNLTTPGGKDSAARSLNKAMVETVXXXXXX 60
AE TRNHLNAGDITYSVRAMD LVGLLDV LRNLTPGGKDSAARSLNKAMVETV
Sbjct: 1 AEQTRNHLNAGDITYSVRAMDQLVGLLDVQLRLNLTTPGGKDSAARSLNKAMVETVNNLLQP 60

Query: 61 XXXXXWRDLTTSNDLRAATMLLHTVEESAFVLADNLLKTDIVRENTDNIKLEVARLSTEG 120
WRDLTTSND LRAATMLLHTVEESAFVLADNLLKTDIVRENTDNIKLEVARLSTEG
Sbjct: 61 QALNAWRDLTTSNDQLRAATMLLHTVEESAFVLADNLLKTDIVRENTDNIKLEVARLSTEG 120

☐ >[gi|14149677|ref|NP_056051.1|](#) lectomedin-3 [Homo sapiens]
[gi|11037016|gb|AAG27462.1|AF307080.1](#) lectomedin-3 [Homo sapiens]
Length = 1240

Score = 202 bits (515), Expect = 5e-52
Identities = 105/133 (78%), Positives = 105/133 (78%), Gaps = 13/133 (9%)

Query: 1 AENTRNHLNAGDITYSVRAMDNLVGLLDVNLRLNLTTPGGKDSAARSLNK----- 48
AE TRNHLNAGDITYSVRAMD LVGLLDV LRNLTPGGKDSAARSLNK
Sbjct: 576 AEQTRNHLNAGDITYSVRAMDQLVGLLDVQLRLNLTTPGGKDSAARSLNKLQKRERSCRAYV 635

Query: 49 -AMVETVXXXXXXXXXXXXWRDLTTSNDLRAATMLLHTVEESAFVLADNLLKTDIVRENTD 107
AMVETV WRDLTTSND LRAATMLLHTVEESAFVLADNLLKTDIVRENTD
Sbjct: 636 QAMVETVNNLLQPQALNAWRDLTTSNDQLRAATMLLHTVEESAFVLADNLLKTDIVRENTD 695

Query: 108 NIKLEVARLSTEG 120
NIKLEVARLSTEG
Sbjct: 696 NIKLEVARLSTEG 708

☐ >[gi|7513950|pir|T17199](#) CL3BB protein - rat
[gi|3695143|gb|AAC62664.1|](#) CL3BB [Rattus norvegicus]
Length = 1298

Score = 199 bits (506), Expect = 6e-51
Identities = 103/133 (77%), Positives = 104/133 (78%), Gaps = 13/133 (9%)

Query: 1 AENTRNHLNAGDITYSVRAMDNLVGLLDVNLRLNLTTPGGKDSAARSLNK----- 48
AE TRNHLNAGDITYSVRAMD LVGLLDV LRNLTPGGKDSAARSLNK
Sbjct: 643 AEQTRNHLNAGDITYSVRAMDQLVGLLDVQLRLNLTTPGGKDSAARSLNKLQKRERSCRAYV 702

Query: 49 -AMVETVXXXXXXXXXXXXWRDLTTSNDLRAATMLLHTVEESAFVLADNLLKTDIVRENTD 107
AMVETV WRDLTTSND LRAATMLL TVEESAFVLADNLLKTDIVRENTD
Sbjct: 703 QAMVETVNNLLQPQALNAWRDLTTSNDQLRAATMLLD TVEESAFVLADNLLKTDIVRENTD 762

Query: 108 NIKLEVARLSTEG 120
NI+LEVARLSTEG
Sbjct: 763 NIQLEVARLSTEG 775

☐ >[gi|7513509|pir|T18398](#) latrophilin-3, splice variant bbag, brain-specific - bov
[gi|4164067|gb|AAD05328.1|](#) latrophilin 3 splice variant bbag [Bos taurus]

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Length = 1299

Score = 199 bits (505), Expect = 8e-51

Identities = 103/133 (77%), Positives = 104/133 (78%), Gaps = 13/133 (9%)

Query: 1 AENTRNHLNAGDITYSVRAMDNLVGLLDVNLRLNLTGGKDSAARSLNK----- 48
 AE TRNHLNAGDITYSVRAMD LVGLLDV LRNLTPGGKDSAARSLNK
 Sbjct: 644 AEQTRNHLNAGDITYSVRAMDQLVGLLDVQLRLNLTGGKDSAARSLNKLQKRERSCRAYV 703

Query: 49 -AMVETVXXXXXXXXXXXXWRDLTTSNLRATMLLHTVEESAFVLADNLLKTDIVRENTD 107
 AMVETV WRDLTTSN LRAATMLL TVEESAFVLADNLLKTDIVRENTD
 Sbjct: 704 QAMVETVNNLLQPQALNAWRDLTTSNQLRAATMLLDTVEESAFVLADNLLKTDIVRENTD 763

Query: 108 NIKLEVARLSTEG 120
 NI+LEVARLSTEG
 Sbjct: 764 NIQLEVARLSTEG 776

☐ >gi|7513512|pir|T18408 latrophilin-3, splice variant bbbg, brain-specific - bov
 gi|4164073|gb|AAD05331.1| latrophilin 3 splice variant bbbg [Bos taurus]
 Length = 1308

Score = 199 bits (505), Expect = 8e-51

Identities = 103/133 (77%), Positives = 104/133 (78%), Gaps = 13/133 (9%)

Query: 1 AENTRNHLNAGDITYSVRAMDNLVGLLDVNLRLNLTGGKDSAARSLNK----- 48
 AE TRNHLNAGDITYSVRAMD LVGLLDV LRNLTPGGKDSAARSLNK
 Sbjct: 644 AEQTRNHLNAGDITYSVRAMDQLVGLLDVQLRLNLTGGKDSAARSLNKLQKRERSCRAYV 703

Query: 49 -AMVETVXXXXXXXXXXXXWRDLTTSNLRATMLLHTVEESAFVLADNLLKTDIVRENTD 107
 AMVETV WRDLTTSN LRAATMLL TVEESAFVLADNLLKTDIVRENTD
 Sbjct: 704 QAMVETVNNLLQPQALNAWRDLTTSNQLRAATMLLDTVEESAFVLADNLLKTDIVRENTD 763

Query: 108 NIKLEVARLSTEG 120
 NI+LEVARLSTEG
 Sbjct: 764 NIQLEVARLSTEG 776

☐ >gi|7513951|pir|T17200 CL3BC protein - rat
 gi|3695145|gb|AAC62665.1| CL3BC [Rattus norvegicus]
 Length = 1341

Score = 198 bits (503), Expect = 1e-50

Identities = 103/133 (77%), Positives = 104/133 (78%), Gaps = 13/133 (9%)

Query: 1 AENTRNHLNAGDITYSVRAMDNLVGLLDVNLRLNLTGGKDSAARSLNK----- 48
 AE TRNHLNAGDITYSVRAMD LVGLLDV LRNLTPGGKDSAARSLNK
 Sbjct: 643 AEQTRNHLNAGDITYSVRAMDQLVGLLDVQLRLNLTGGKDSAARSLNKLQKRERSCRAYV 702

Query: 49 -AMVETVXXXXXXXXXXXXWRDLTTSNLRATMLLHTVEESAFVLADNLLKTDIVRENTD 107
 AMVETV WRDLTTSN LRAATMLL TVEESAFVLADNLLKTDIVRENTD
 Sbjct: 703 QAMVETVNNLLQPQALNAWRDLTTSNQLRAATMLLDTVEESAFVLADNLLKTDIVRENTD 762

Query: 108 NIKLEVARLSTEG 120
 NI+LEVARLSTEG
 Sbjct: 763 NIQLEVARLSTEG 775

☐ >gi|7513510|pir|T18405 latrophilin-3, splice variant bbah, brain-specific - bov
 gi|4164069|gb|AAD05329.1| latrophilin 3 splice variant bbah [Bos taurus]
 Length = 1342

Score = 198 bits (503), Expect = 1e-50

Identities = 103/133 (77%), Positives = 104/133 (78%), Gaps = 13/133 (9%)

Query: 1 AENTRNHLNAGDITYSVRAMDNLVGLLDVNLRLNLTGGKDSAARSLNK----- 48
 AE TRNHLNAGDITYSVRAMD LVGLLDV LRNLTPGGKDSAARSLNK

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Sbjct: 644 AEQTRNHLNAGDITYSVRAMDQLVGLLDVQLRNLTTPGGKDSAARSLNKLQKRERSCRAYV 703

Query: 49 -AMVETVXXXXXXXXXXXXWRDLTTSNLRATMMLHTVEESAFVLADNLLKTDIVRENTD 107
AMVETV WRDLTTSN LRAATMLL TVEESAFVLADNLLKTDIVRENTD

Sbjct: 704 QAMVETVNNLLQPQALNAWRDLTTSNQLRAATMLLDVEESAFVLADNLLKTDIVRENTD 763

Query: 108 NIKLEVARLSTEG 120
NI+LEVARLSTEG

Sbjct: 764 NIQLEVARLSTEG 776

☐ >gi|7513513|pir|T18409 latrophilin-3, splice variant bbbh, brain-specific - bov
gi|4164075|gb|AAD05332.1| latrophilin 3 splice variant bbbh [Bos taurus]
Length = 1351

Score = 198 bits (503), Expect = 1e-50
Identities = 103/133 (77%), Positives = 104/133 (78%), Gaps = 13/133 (9%)

Query: 1 AENTRNHLNAGDITYSVRAMDNLVGLLDVNLRLNLTTPGGKDSAARSLNK----- 48
AE TRNHLNAGDITYSVRAMD LVGLLDV LRNLTPGGKDSAARSLNK
Sbjct: 644 AEQTRNHLNAGDITYSVRAMDQLVGLLDVQLRNLTTPGGKDSAARSLNKLQKRERSCRAYV 703

Query: 49 -AMVETVXXXXXXXXXXXXWRDLTTSNLRATMMLHTVEESAFVLADNLLKTDIVRENTD 107
AMVETV WRDLTTSN LRAATMLL TVEESAFVLADNLLKTDIVRENTD

Sbjct: 704 QAMVETVNNLLQPQALNAWRDLTTSNQLRAATMLLDVEESAFVLADNLLKTDIVRENTD 763

Query: 108 NIKLEVARLSTEG 120
NI+LEVARLSTEG

Sbjct: 764 NIQLEVARLSTEG 776

☐ >gi|7513947|pir|T17187 CL3AB protein - rat
gi|3695137|gb|AAC62661.1| CL3AB [Rattus norvegicus]
Length = 1230

Score = 198 bits (503), Expect = 1e-50
Identities = 103/133 (77%), Positives = 104/133 (78%), Gaps = 13/133 (9%)

Query: 1 AENTRNHLNAGDITYSVRAMDNLVGLLDVNLRLNLTTPGGKDSAARSLNK----- 48
AE TRNHLNAGDITYSVRAMD LVGLLDV LRNLTPGGKDSAARSLNK
Sbjct: 575 AEQTRNHLNAGDITYSVRAMDQLVGLLDVQLRNLTTPGGKDSAARSLNKLQKRERSCRAYV 634

Query: 49 -AMVETVXXXXXXXXXXXXWRDLTTSNLRATMMLHTVEESAFVLADNLLKTDIVRENTD 107
AMVETV WRDLTTSN LRAATMLL TVEESAFVLADNLLKTDIVRENTD

Sbjct: 635 QAMVETVNNLLQPQALNAWRDLTTSNQLRAATMLLDVEESAFVLADNLLKTDIVRENTD 694

Query: 108 NIKLEVARLSTEG 120
NI+LEVARLSTEG

Sbjct: 695 NIQLEVARLSTEG 707

☐ >gi|7513506|pir|T18393 latrophilin-3, splice variant abbg, brain-specific - bov
gi|4164061|gb|AAD05325.1| latrophilin 3 splice variant abbg [Bos taurus]
Length = 1240

Score = 197 bits (502), Expect = 2e-50
Identities = 103/133 (77%), Positives = 104/133 (78%), Gaps = 13/133 (9%)

Query: 1 AENTRNHLNAGDITYSVRAMDNLVGLLDVNLRLNLTTPGGKDSAARSLNK----- 48
AE TRNHLNAGDITYSVRAMD LVGLLDV LRNLTPGGKDSAARSLNK
Sbjct: 576 AEQTRNHLNAGDITYSVRAMDQLVGLLDVQLRNLTTPGGKDSAARSLNKLQKRERSCRAYV 635

Query: 49 -AMVETVXXXXXXXXXXXXWRDLTTSNLRATMMLHTVEESAFVLADNLLKTDIVRENTD 107
AMVETV WRDLTTSN LRAATMLL TVEESAFVLADNLLKTDIVRENTD

Sbjct: 636 QAMVETVNNLLQPQALNAWRDLTTSNQLRAATMLLDVEESAFVLADNLLKTDIVRENTD 695

Query: 108 NIKLEVARLSTEG 120

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NI+LEVARLSTEG

Sbjct: 696 NIQLEVARLSTEG 708

☐ >gi|7513503|pir|T18390 latrophilin-3, splice variant abag, brain-specific - bov
 gi|4164055|gb|AAD05322.1| latrophilin 3 splice variant abag [Bos taurus]
 Length = 1231

Score = 197 bits (502), Expect = 2e-50

Identities = 103/133 (77%), Positives = 104/133 (78%), Gaps = 13/133 (9%)

Query: 1 AENTRNHLNAGDITYSVRAMDNLVGLLDVNLRLNLTTPGGKDSAARSLNK----- 48
 AE TRNHLNAGDITYSVRAMD LVGLLDV LRNLTPGGKDSAARSLNK
 Sbjct: 576 AEQTRNHLNAGDITYSVRAMDQLVGLLDVQLRLNLTTPGGKDSAARSLNKLQKRERSCRAYV 635

Query: 49 -AMVETVXXXXXXXXXXXXWRDLTTSNLRATMLLHTVEESAFVLADNLLKTDIVRENTD 107
 AMVETV WRDLTTSN LRAATMLL TVEESAFVLADNLLKTDIVRENTD
 Sbjct: 636 QAMVETVNNLLQPQALNAWRDLTTSNQLRAATMLLD TVEESAFVLADNLLKTDIVRENTD 695

Query: 108 NIKLEVARLSTEG 120
 NI+LEVARLSTEG
 Sbjct: 696 NIQLEVARLSTEG 708

☐ >gi|7513948|pir|T17188 CL3AC protein - rat
 gi|3695139|gb|AAC62662.1| CL3AC [Rattus norvegicus]
 Length = 1273

Score = 197 bits (501), Expect = 2e-50

Identities = 103/133 (77%), Positives = 104/133 (78%), Gaps = 13/133 (9%)

Query: 1 AENTRNHLNAGDITYSVRAMDNLVGLLDVNLRLNLTTPGGKDSAARSLNK----- 48
 AE TRNHLNAGDITYSVRAMD LVGLLDV LRNLTPGGKDSAARSLNK
 Sbjct: 575 AEQTRNHLNAGDITYSVRAMDQLVGLLDVQLRLNLTTPGGKDSAARSLNKLQKRERSCRAYV 634

Query: 49 -AMVETVXXXXXXXXXXXXWRDLTTSNLRATMLLHTVEESAFVLADNLLKTDIVRENTD 107
 AMVETV WRDLTTSN LRAATMLL TVEESAFVLADNLLKTDIVRENTD
 Sbjct: 635 QAMVETVNNLLQPQALNAWRDLTTSNQLRAATMLLD TVEESAFVLADNLLKTDIVRENTD 694

Query: 108 NIKLEVARLSTEG 120
 NI+LEVARLSTEG
 Sbjct: 695 NIQLEVARLSTEG 707

☐ >gi|7513504|pir|T18391 latrophilin-3, splice variant abah, brain-specific - bov
 gi|4164057|gb|AAD05323.1| latrophilin 3 splice variant abah [Bos taurus]
 Length = 1274

Score = 197 bits (501), Expect = 2e-50

Identities = 103/133 (77%), Positives = 104/133 (78%), Gaps = 13/133 (9%)

Query: 1 AENTRNHLNAGDITYSVRAMDNLVGLLDVNLRLNLTTPGGKDSAARSLNK----- 48
 AE TRNHLNAGDITYSVRAMD LVGLLDV LRNLTPGGKDSAARSLNK
 Sbjct: 576 AEQTRNHLNAGDITYSVRAMDQLVGLLDVQLRLNLTTPGGKDSAARSLNKLQKRERSCRAYV 635

Query: 49 -AMVETVXXXXXXXXXXXXWRDLTTSNLRATMLLHTVEESAFVLADNLLKTDIVRENTD 107
 AMVETV WRDLTTSN LRAATMLL TVEESAFVLADNLLKTDIVRENTD
 Sbjct: 636 QAMVETVNNLLQPQALNAWRDLTTSNQLRAATMLLD TVEESAFVLADNLLKTDIVRENTD 695

Query: 108 NIKLEVARLSTEG 120
 NI+LEVARLSTEG
 Sbjct: 696 NIQLEVARLSTEG 708

☐ >gi|7513507|pir|T18394 latrophilin-3, splice variant abbh, brain-specific - bov
 gi|4164063|gb|AAD05326.1| latrophilin 3 splice variant abbh [Bos taurus]
 Length = 1283

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Score = 197 bits (501), Expect = 2e-50
Identities = 103/133 (77%), Positives = 104/133 (78%), Gaps = 13/133 (9%)

Query: 1 AENTRNHLNAGDITYSVRAMDNLVGLLDVNLRLNLTTPGGKDSAARSLNK----- 48
AE TRNHLNAGDITYSVRAMD LVGLLDV LRNLTPGGKDSAARSLNK
Sbjct: 576 AEQTRNHLNAGDITYSVRAMDQLVGLLDVQLRLNLTTPGGKDSAARSLNKLQKRERSCRAYV 635

Query: 49 -AMVETVXXXXXXXXXXXXWRDLTTSNLRATMLLHTVEESAFVLADNLLKTDIVRENTD 107
AMVETV WRDLTTS LRAATMLL TVEESAFVLADNLLKTDIVRENTD
Sbjct: 636 QAMVETVNNLLQPQALNAWRDLTTSQDLRAATMLLD TVEESAFVLADNLLKTDIVRENTD 695

Query: 108 NIKLEVARLSTEG 120
NI+LEVARLSTEG
Sbjct: 696 NIQLEVARLSTEG 708

☐ >gi|18677755|ref|NP_570835.1| calcium-independent alpha-latrotoxin receptor hom
lectomedin-3 [Rattus norvegicus]
gi|7513906|pir||T14327 alpha-latrotoxin receptor 3, calcium-independent - rat
gi|3882981|gb|AAC77816.1| calcium-independent alpha-latrotoxin receptor homolog
norvegicus]
Length = 1550

Score = 196 bits (499), Expect = 4e-50
Identities = 103/133 (77%), Positives = 104/133 (78%), Gaps = 13/133 (9%)

Query: 1 AENTRNHLNAGDITYSVRAMDNLVGLLDVNLRLNLTTPGGKDSAARSLNK----- 48
AE TRNHLNAGDITYSVRAMD LVGLLDV LRNLTPGGKDSAARSLNK
Sbjct: 643 AEQTRNHLNAGDITYSVRAMDQLVGLLDVQLRLNLTTPGGKDSAARSLNKLQKRERSCRAYV 702

Query: 49 -AMVETVXXXXXXXXXXXXWRDLTTSNLRATMLLHTVEESAFVLADNLLKTDIVRENTD 107
AMVETV WRDLTTS LRAATMLL TVEESAFVLADNLLKTDIVRENTD
Sbjct: 703 QAMVETVNNLLQPQALNAWRDLTTSQDLRAATMLLD TVEESAFVLADNLLKTDIVRENTD 762

Query: 108 NIKLEVARLSTEG 120
NI+LEVARLSTEG
Sbjct: 763 NIQLEVARLSTEG 775

☐ >gi|7513949|pir||T17198 CL3BA protein - rat
gi|3695141|gb|AAC62663.1| CL3BA [Rattus norvegicus]
Length = 1527

Score = 196 bits (497), Expect = 6e-50
Identities = 103/133 (77%), Positives = 104/133 (78%), Gaps = 13/133 (9%)

Query: 1 AENTRNHLNAGDITYSVRAMDNLVGLLDVNLRLNLTTPGGKDSAARSLNK----- 48
AE TRNHLNAGDITYSVRAMD LVGLLDV LRNLTPGGKDSAARSLNK
Sbjct: 643 AEQTRNHLNAGDITYSVRAMDQLVGLLDVQLRLNLTTPGGKDSAARSLNKLQKRERSCRAYV 702

Query: 49 -AMVETVXXXXXXXXXXXXWRDLTTSNLRATMLLHTVEESAFVLADNLLKTDIVRENTD 107
AMVETV WRDLTTS LRAATMLL TVEESAFVLADNLLKTDIVRENTD
Sbjct: 703 QAMVETVNNLLQPQALNAWRDLTTSQDLRAATMLLD TVEESAFVLADNLLKTDIVRENTD 762

Query: 108 NIKLEVARLSTEG 120
NI+LEVARLSTEG
Sbjct: 763 NIQLEVARLSTEG 775

☐ >gi|7513508|pir||T18395 latrophilin-3, splice variant bbaf, brain-specific - bov
gi|4164065|gb|AAD05327.1| latrophilin 3 splice variant bbaf [Bos taurus]
Length = 1571

Score = 195 bits (496), Expect = 9e-50
Identities = 103/133 (77%), Positives = 104/133 (78%), Gaps = 13/133 (9%)

Query: 1 AENTRNHLNAGDITYSVRAMDNLVGLLDVNLRLNLTTPGGKDSAARSLNK----- 48

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AE TRNHLNAGDITYSVRAMD LVGLLDV LRNLTPGGKDSAARSLNK
 Sbjct: 644 AEQTRNHLNAGDITYSVRAMDQLVGLLDVQLRNLTTPGGKDSAARSLNKLQKRERSCRAYV 703

Query: 49 -AMVETVXXXXXXXXXXXXWRDLTTSNLRATMMLHTVEESAFVLADNLLKTDIVRENTD 107
 AMVETV WRDLTTSN LRAATMLL TVEESAFVLADNLLKTDIVRENTD

Sbjct: 704 QAMVETVNNLLQPQALNAWRDLTTSNQLRAATMLLDTVEESAFVLADNLLKTDIVRENTD 763

Query: 108 NIKLEVARLSTEG 120
 NI+LEVARLSTEG

Sbjct: 764 NIQLEVARLSTEG 776

☐ >gi|7513511|pir|T18407 latrophilin-3, splice variant bbbf, brain-specific - bov
 gi|4164071|gb|AAD05330.1| latrophilin 3 splice variant bbbf [Bos taurus]
 Length = 1580

Score = 195 bits (495), Expect = 1e-49
 Identities = 103/133 (77%), Positives = 104/133 (78%), Gaps = 13/133 (9%)

Query: 1 AENTRNHLNAGDITYSVRAMDNLVGLLDVNLNRNLTPGGKDSAARSLNK----- 48
 AE TRNHLNAGDITYSVRAMD LVGLLDV LRNLTPGGKDSAARSLNK

Sbjct: 644 AEQTRNHLNAGDITYSVRAMDQLVGLLDVQLRNLTTPGGKDSAARSLNKLQKRERSCRAYV 703

Query: 49 -AMVETVXXXXXXXXXXXXWRDLTTSNLRATMMLHTVEESAFVLADNLLKTDIVRENTD 107
 AMVETV WRDLTTSN LRAATMLL TVEESAFVLADNLLKTDIVRENTD

Sbjct: 704 QAMVETVNNLLQPQALNAWRDLTTSNQLRAATMLLDTVEESAFVLADNLLKTDIVRENTD 763

Query: 108 NIKLEVARLSTEG 120
 NI+LEVARLSTEG

Sbjct: 764 NIQLEVARLSTEG 776

☐ >gi|7513946|pir|T17186 CL3AA protein - rat
 gi|3695135|gb|AAC62660.1| CL3AA [Rattus norvegicus]
 Length = 1459

Score = 194 bits (494), Expect = 1e-49
 Identities = 103/133 (77%), Positives = 104/133 (78%), Gaps = 13/133 (9%)

Query: 1 AENTRNHLNAGDITYSVRAMDNLVGLLDVNLNRNLTPGGKDSAARSLNK----- 48
 AE TRNHLNAGDITYSVRAMD LVGLLDV LRNLTPGGKDSAARSLNK

Sbjct: 575 AEQTRNHLNAGDITYSVRAMDQLVGLLDVQLRNLTTPGGKDSAARSLNKLQKRERSCRAYV 634

Query: 49 -AMVETVXXXXXXXXXXXXWRDLTTSNLRATMMLHTVEESAFVLADNLLKTDIVRENTD 107
 AMVETV WRDLTTSN LRAATMLL TVEESAFVLADNLLKTDIVRENTD

Sbjct: 635 QAMVETVNNLLQPQALNAWRDLTTSNQLRAATMLLDTVEESAFVLADNLLKTDIVRENTD 694

Query: 108 NIKLEVARLSTEG 120
 NI+LEVARLSTEG

Sbjct: 695 NIQLEVARLSTEG 707

☐ >gi|7513502|pir|T18389 latrophilin-3, splice variant abaf, brain-specific - bov
 gi|4164053|gb|AAD05321.1| latrophilin 3 splice variant abaf [Bos taurus]
 Length = 1503

Score = 194 bits (493), Expect = 2e-49
 Identities = 103/133 (77%), Positives = 104/133 (78%), Gaps = 13/133 (9%)

Query: 1 AENTRNHLNAGDITYSVRAMDNLVGLLDVNLNRNLTPGGKDSAARSLNK----- 48
 AE TRNHLNAGDITYSVRAMD LVGLLDV LRNLTPGGKDSAARSLNK

Sbjct: 576 AEQTRNHLNAGDITYSVRAMDQLVGLLDVQLRNLTTPGGKDSAARSLNKLQKRERSCRAYV 635

Query: 49 -AMVETVXXXXXXXXXXXXWRDLTTSNLRATMMLHTVEESAFVLADNLLKTDIVRENTD 107
 AMVETV WRDLTTSN LRAATMLL TVEESAFVLADNLLKTDIVRENTD

Sbjct: 636 QAMVETVNNLLQPQALNAWRDLTTSNQLRAATMLLDTVEESAFVLADNLLKTDIVRENTD 695

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Query: 108 NIKLEVARLSTEG 120
 NI+LEVARLSTEG
 Sbjct: 696 NIQLEVARLSTEG 708

☐ >gi|7513505|pir|T18392 latrophilin-3, splice variant abbf, brain-specific - bov
 gi|4164059|gb|AAD05324.1| latrophilin 3 splice variant abbf [Bos taurus]
 Length = 1512

Score = 194 bits (493), Expect = 2e-49
 Identities = 103/133 (77%), Positives = 104/133 (78%), Gaps = 13/133 (9%)

Query: 1 AENTRNHLNAGDITYSVRAMDNLVGLLDVNLRLNLTGGKDSAARSLNK----- 48
 AE TRNHLNAGDITYSVRAMD LVGLLDV LRNLTPGGKDSAARSLNK
 Sbjct: 576 AEQTRNHLNAGDITYSVRAMDQLVGLLDVQLRLNLTGGKDSAARSLNKLQKRERSCRAYV 635

Query: 49 -AMVETVXXXXXXXXXXXXWRDLTTSNLRATMLLHTVEESAFVLADNLLKTDIVRENTD 107
 AMVETV WRDLTTSN LRATMLL TVEESAFVLADNLLKTDIVRENTD
 Sbjct: 636 QAMVETVNNLLQPQALNAWRDLTTSNQLRAATMLLDVEESAFVLADNLLKTDIVRENTD 695

Query: 108 NIKLEVARLSTEG 120
 NI+LEVARLSTEG
 Sbjct: 696 NIQLEVARLSTEG 708

☐ >gi|7021080|dbj|BAA91375.1| unnamed protein product [Homo sapiens]
 Length = 393

Score = 150 bits (380), Expect = 2e-36
 Identities = 77/92 (83%), Positives = 77/92 (83%)

Query: 1 AENTRNHLNAGDITYSVRAMDNLVGLLDVNLRLNLTGGKDSAARSLNKAMVETVXXXXXX 60
 AE TRNHLNAGDITYSVRAMD LVGLLDV LRNLTPGGKDSAARSLNKAMVETV
 Sbjct: 262 AEQTRNHLNAGDITYSVRAMDQLVGLLDVQLRLNLTGGKDSAARSLNKAMVETVNNLLQP 321

Query: 61 XXXXXWRDLTTSNLRATMLLHTVEESAFVL 92
 WRDLTTSN LRATMLLHTVEESAFVL
 Sbjct: 322 QALNAWRDLTTSNQLRAATMLLHTVEESAFVL 353

☐ >gi|5880492|gb|AAD54676.1|AF104938.1 lectomedin-1 beta [Homo sapiens]
 Length = 1123

Score = 114 bits (286), Expect = 2e-25
 Identities = 60/120 (50%), Positives = 78/120 (65%)

Query: 1 AENTRNHLNAGDITYSVRAMDNLVGLLDVNLRLNLTGGKDSAARSLNKAMVETVXXXXXX 60
 A++T+ + AGD++ SVR M+ LV +LD L+ L P KDSA RS NKA+V+TV
 Sbjct: 547 AKHTKGPVFAGDVSSSVRLMEQLVDILDAQLQELKPSEKDSAGRSYNKAIVDTVDNLLRP 606

Query: 61 XXXXXWRDLTTSNLRATMLLHTVEESAFVLADNLLKTDIVRENTDNIKLEVARLSTEG 120
 W+ + +S+ ATMLL T+EE AFVLADNLL+ V T+NI LEVA LSTEG
 Sbjct: 607 EALESWKHMNSSEQAHTATMLLDLTLEEGAFVLADNLLLEPTRVSMPTENIVLEVAVLSTEG 666

☐ >gi|5880490|gb|AAD54675.1|AF104266.1 lectomedin-1 alpha [Homo sapiens]
 Length = 1177

Score = 114 bits (286), Expect = 2e-25
 Identities = 60/120 (50%), Positives = 78/120 (65%)

Query: 1 AENTRNHLNAGDITYSVRAMDNLVGLLDVNLRLNLTGGKDSAARSLNKAMVETVXXXXXX 60
 A++T+ + AGD++ SVR M+ LV +LD L+ L P KDSA RS NKA+V+TV
 Sbjct: 547 AKHTKGPVFAGDVSSSVRLMEQLVDILDAQLQELKPSEKDSAGRSYNKAIVDTVDNLLRP 606

Query: 61 XXXXXWRDLTTSNLRATMLLHTVEESAFVLADNLLKTDIVRENTDNIKLEVARLSTEG 120
 W+ + +S+ ATMLL T+EE AFVLADNLL+ V T+NI LEVA LSTEG
 Sbjct: 607 EALESWKHMNSSEQAHTATMLLDLTLEEGAFVLADNLLLEPTRVSMPTENIVLEVAVLSTEG 666

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☐ >gi|6912464|ref|NP_036434.1| latrophilin 1; KIAA0786 protein; lectomedin-1; lat sapiens]
 gi|4034486|emb|CAA10458.1| latrophilin-2 [Homo sapiens]
 gi|5880494|gb|AAD54677.1|AF104939.1 lectomedin-1 gamma [Homo sapiens]
 gi|6274511|emb|CAB60229.1| latrophilin-2 [Homo sapiens]
 Length = 1403

Score = 114 bits (284), Expect = 3e-25
 Identities = 60/120 (50%), Positives = 78/120 (65%)

Query: 1 AENTRNHLNAGDITYSVRAMDNLVGLLDVNLRLNLTGGKDSAARSLNKAMVETVXXXXXX 60
 A++T+ + AGD++ SVR M+ LV +LD L+ L P KDSA RS NKA+V+TV
 Sbjct: 547 AKHTKGPVFAGDVSSSVRLMEQLVDILDAQLQELKPSEKDSAGRSYNKAIVDTVDNLLRP 606
 Query: 61 XXXXXWRDLTTSNLRRAATMLLHTVEESAFVLADNLLKTDIVRENTDNIKLEVARLSTEG 120
 W+ + +S+ ATMLL T+EE AFVLADNLL+ V T+NI LEVA LSTEG
 Sbjct: 607 EALESWKHMNSSEQAHTATMLLDLTLEEGAFVLADNLLPEPTRVSMPTENIVLEVAVLSTEG 666

☐ >gi|7513501|pir|T18383 latrophilin-2, splice variant bbabe - bovine
 gi|4164041|gb|AAD05315.1| Latrophilin 2 splice variant bbabe [Bos taurus]
 Length = 1422

Score = 112 bits (280), Expect = 8e-25
 Identities = 59/120 (49%), Positives = 78/120 (65%)

Query: 1 AENTRNHLNAGDITYSVRAMDNLVGLLDVNLRLNLTGGKDSAARSLNKAMVETVXXXXXX 60
 A++T+ + AGD++ SVR M+ LV +LD L+ L P KDSA RS NKA+V+TV
 Sbjct: 551 AKHTKGPVFAGDVSSSVRLMEQLVDILDAQLQELKPSEKDSAGRSYNKAIVDTVDNLLRP 610
 Query: 61 XXXXXWRDLTTSNLRRAATMLLHTVEESAFVLADNLLKTDIVRENTDNIKLEVARLSTEG 120
 W+ + +S+ ATMLL T+EE AFVLADNLL+ V T+NI LEVA LSTEG
 Sbjct: 611 EALESWKHMNSSEQAHTATMLLDLTLEEGAFVLADNLLPEPTRVSMPTENIVLEVAVLSTEG 670

☐ >gi|7513491|pir|T18381 latrophilin-2 (splice variant bbaae) - bovine
 gi|4164037|gb|AAD05313.1| latrophilin 2 splice variant bbaae [Bos taurus]
 Length = 1407

Score = 112 bits (280), Expect = 8e-25
 Identities = 59/120 (49%), Positives = 78/120 (65%)

Query: 1 AENTRNHLNAGDITYSVRAMDNLVGLLDVNLRLNLTGGKDSAARSLNKAMVETVXXXXXX 60
 A++T+ + AGD++ SVR M+ LV +LD L+ L P KDSA RS NKA+V+TV
 Sbjct: 551 AKHTKGPVFAGDVSSSVRLMEQLVDILDAQLQELKPSEKDSAGRSYNKAIVDTVDNLLRP 610
 Query: 61 XXXXXWRDLTTSNLRRAATMLLHTVEESAFVLADNLLKTDIVRENTDNIKLEVARLSTEG 120
 W+ + +S+ ATMLL T+EE AFVLADNLL+ V T+NI LEVA LSTEG
 Sbjct: 611 EALESWKHMNSSEQAHTATMLLDLTLEEGAFVLADNLLPEPTRVSMPTENIVLEVAVLSTEG 670

☐ >gi|7513498|pir|T18301 latrophilin-2, splice variant baaae - bovine
 gi|4164021|gb|AAD05305.1| latrophilin 2 splice variant baaae [Bos taurus]
 Length = 1341

Score = 112 bits (280), Expect = 9e-25
 Identities = 59/120 (49%), Positives = 78/120 (65%)

Query: 1 AENTRNHLNAGDITYSVRAMDNLVGLLDVNLRLNLTGGKDSAARSLNKAMVETVXXXXXX 60
 A++T+ + AGD++ SVR M+ LV +LD L+ L P KDSA RS NKA+V+TV
 Sbjct: 485 AKHTKGPVFAGDVSSSVRLMEQLVDILDAQLQELKPSEKDSAGRSYNKAIVDTVDNLLRP 544
 Query: 61 XXXXXWRDLTTSNLRRAATMLLHTVEESAFVLADNLLKTDIVRENTDNIKLEVARLSTEG 120
 W+ + +S+ ATMLL T+EE AFVLADNLL+ V T+NI LEVA LSTEG
 Sbjct: 545 EALESWKHMNSSEQAHTATMLLDLTLEEGAFVLADNLLPEPTRVSMPTENIVLEVAVLSTEG 604

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☐ >gi|7513500|pir|T18367 latrophilin-2, splice variant baabe - bovine
 gi|4164025|gb|AAD05307.1| latrophilin 2 splice variant baabe [Bos taurus]
 Length = 1356

Score = 112 bits (280), Expect = 9e-25
 Identities = 59/120 (49%), Positives = 78/120 (65%)

Query: 1 AENTRNHLNAGDITYSVRAMDNLVGLLDVNLRLNLTGGKDSAARSLNKAMVETVXXXXXX 60
 A++T+ + AGD++ SVR M+ LV +LD L+ L P KDSA RS NKA+V+TV
 Sbjct: 485 AKHTKGPVFAGDVSSSVRLMEQLVDILDAQLQELKPSEKDSAGRSYNKAIVDTVNDLLRP 544

Query: 61 XXXXXWRDLTTSNDLRAATMLLHTVEESAFVLADNLLKTDIVRENTDNIKLEVARLSTEG 120
 W+ + +S+ ATMLL T+EE AFVLADNL++ V T+NI LEVA LSTEG
 Sbjct: 545 EALESWKHMNSSEQAHTATMLLDTLEEGAFVLADNLVEPTRVSMPTENIVLEVAVLSTEG 604

☐ >gi|7513492|pir|T18382 latrophilin-2 (splice variant bbaaf) - bovine
 gi|4164039|gb|AAD05314.1| latrophilin 2 splice variant bbaaf [Bos taurus]
 Length = 1450

Score = 112 bits (280), Expect = 1e-24
 Identities = 59/120 (49%), Positives = 78/120 (65%)

Query: 1 AENTRNHLNAGDITYSVRAMDNLVGLLDVNLRLNLTGGKDSAARSLNKAMVETVXXXXXX 60
 A++T+ + AGD++ SVR M+ LV +LD L+ L P KDSA RS NKA+V+TV
 Sbjct: 551 AKHTKGPVFAGDVSSSVRLMEQLVDILDAQLQELKPSEKDSAGRSYNKAIVDTVNDLLRP 610

Query: 61 XXXXXWRDLTTSNDLRAATMLLHTVEESAFVLADNLLKTDIVRENTDNIKLEVARLSTEG 120
 W+ + +S+ ATMLL T+EE AFVLADNL++ V T+NI LEVA LSTEG
 Sbjct: 611 EALESWKHMNSSEQAHTATMLLDTLEEGAFVLADNLVEPTRVSMPTENIVLEVAVLSTEG 670

☐ >gi|7513493|pir|T18384 latrophilin-2 (splice variant bbabf) - bovine
 gi|4164043|gb|AAD05316.1| latrophilin 2 splice variant bbabf [Bos taurus]
 Length = 1465

Score = 112 bits (280), Expect = 1e-24
 Identities = 59/120 (49%), Positives = 78/120 (65%)

Query: 1 AENTRNHLNAGDITYSVRAMDNLVGLLDVNLRLNLTGGKDSAARSLNKAMVETVXXXXXX 60
 A++T+ + AGD++ SVR M+ LV +LD L+ L P KDSA RS NKA+V+TV
 Sbjct: 551 AKHTKGPVFAGDVSSSVRLMEQLVDILDAQLQELKPSEKDSAGRSYNKAIVDTVNDLLRP 610

Query: 61 XXXXXWRDLTTSNDLRAATMLLHTVEESAFVLADNLLKTDIVRENTDNIKLEVARLSTEG 120
 W+ + +S+ ATMLL T+EE AFVLADNL++ V T+NI LEVA LSTEG
 Sbjct: 611 EALESWKHMNSSEQAHTATMLLDTLEEGAFVLADNLVEPTRVSMPTENIVLEVAVLSTEG 670

☐ >gi|7513486|pir|T18370 latrophilin-2 (splice variant baabf) - bovine
 gi|4164027|gb|AAD05308.1| latrophilin 2 splice variant baabf [Bos taurus]
 Length = 1399

Score = 112 bits (280), Expect = 1e-24
 Identities = 59/120 (49%), Positives = 78/120 (65%)

Query: 1 AENTRNHLNAGDITYSVRAMDNLVGLLDVNLRLNLTGGKDSAARSLNKAMVETVXXXXXX 60
 A++T+ + AGD++ SVR M+ LV +LD L+ L P KDSA RS NKA+V+TV
 Sbjct: 485 AKHTKGPVFAGDVSSSVRLMEQLVDILDAQLQELKPSEKDSAGRSYNKAIVDTVNDLLRP 544

Query: 61 XXXXXWRDLTTSNDLRAATMLLHTVEESAFVLADNLLKTDIVRENTDNIKLEVARLSTEG 120
 W+ + +S+ ATMLL T+EE AFVLADNL++ V T+NI LEVA LSTEG
 Sbjct: 545 EALESWKHMNSSEQAHTATMLLDTLEEGAFVLADNLVEPTRVSMPTENIVLEVAVLSTEG 604

☐ >gi|7513499|pir|T18366 latrophilin-2, splice variant baaaf - bovine
 gi|4164023|gb|AAD05306.1| latrophilin 2 splice variant baaaf [Bos taurus]

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Length = 1384

Score = 112 bits (280), Expect = 1e-24

Identities = 59/120 (49%), Positives = 78/120 (65%)

Query: 1 AENTRNHLNAGDITYSVRAMDNLVGLLDVNLRLNLTGGKDSAARSLNKAMVETVXXXXXX 60
 A++T+ + AGD++ SVR M+ LV +LD L+ L P KDSA RS NKA+V+TV
 Sbjct: 485 AKHTKGPVFAGDVSSSVRLMEQLVDILDAQLQELKPSEKDSAGRSYNKAIVDTVDNLLRP 544

Query: 61 XXXXXWRDLTTSNLRATMMLLHTVEESAFVLADNLLKTDIVRENTDNIKLEVARLSTEG 120
 W+ + +S+ ATMLL T+EE AFVLADNLL+ V T+NI LEVA LSTEG
 Sbjct: 545 EALESWKHMNSSEQAHTATMLLDLTLEEGAFVLADNLEPTRVSMPTENIVLEVAVLSTEG 604

☐ >gi|7513941|pir|T17157 CL2AA protein - rat
 gi|3695123|gb|AAC62654.1| CL2AA [Rattus norvegicus]
 Length = 1452

Score = 106 bits (265), Expect = 6e-23

Identities = 61/133 (45%), Positives = 78/133 (58%), Gaps = 13/133 (9%)

Query: 1 AENTRNHLNAGDITYSVRAMDNLVGLLDVNLRLNLTGGKDSAARSLN----- 47
 A++T+ + AGD++ SVR M+ LV +LD L+ L P KDSA RS N
 Sbjct: 551 AKHTKGTVFAGDVSSSVRLMEQLVDILDAQLQELKPSEKDSAGRSYNKLQKREKTCRAYL 610

Query: 48 KAMVETVXXXXXXXXXXXXWRDLTTSNLRATMMLLHTVEESAFVLADNLLKTDIVRENTD 107
 KA+V+TV W+ + +S+ ATMLL T+EE AFVLADNLL+ V TD
 Sbjct: 611 KAIVDTVDNLLRAETLDCWKHMNSSEQAHTATMLLDLTLEEGAFVLADNLEPTRVSMPTD 670

Query: 108 NIKLEVARLSTEG 120
 NI LEVA LSTEG
 Sbjct: 671 NIVLEVAVLSTEG 683

☐ >gi|11280659|pir|T46611 CL2BB protein - rat
 gi|3695131|gb|AAC62658.1| CL2BB [Rattus norvegicus]
 Length = 1435

Score = 106 bits (264), Expect = 6e-23

Identities = 61/133 (45%), Positives = 78/133 (58%), Gaps = 13/133 (9%)

Query: 1 AENTRNHLNAGDITYSVRAMDNLVGLLDVNLRLNLTGGKDSAARSLN----- 47
 A++T+ + AGD++ SVR M+ LV +LD L+ L P KDSA RS N
 Sbjct: 551 AKHTKGTVFAGDVSSSVRLMEQLVDILDAQLQELKPSEKDSAGRSYNKLQKREKTCRAYL 610

Query: 48 KAMVETVXXXXXXXXXXXXWRDLTTSNLRATMMLLHTVEESAFVLADNLLKTDIVRENTD 107
 KA+V+TV W+ + +S+ ATMLL T+EE AFVLADNLL+ V TD
 Sbjct: 611 KAIVDTVDNLLRAETLDCWKHMNSSEQAHTATMLLDLTLEEGAFVLADNLEPTRVSMPTD 670

Query: 108 NIKLEVARLSTEG 120
 NI LEVA LSTEG
 Sbjct: 671 NIVLEVAVLSTEG 683

☐ >gi|7513942|pir|T17158 CL2AB protein - rat
 gi|3695125|gb|AAC62655.1| CL2AB [Rattus norvegicus]
 Length = 1420

Score = 106 bits (264), Expect = 6e-23

Identities = 61/133 (45%), Positives = 78/133 (58%), Gaps = 13/133 (9%)

Query: 1 AENTRNHLNAGDITYSVRAMDNLVGLLDVNLRLNLTGGKDSAARSLN----- 47
 A++T+ + AGD++ SVR M+ LV +LD L+ L P KDSA RS N
 Sbjct: 551 AKHTKGTVFAGDVSSSVRLMEQLVDILDAQLQELKPSEKDSAGRSYNKLQKREKTCRAYL 610

Query: 48 KAMVETVXXXXXXXXXXXXWRDLTTSNLRATMMLLHTVEESAFVLADNLLKTDIVRENTD 107
 KA+V+TV W+ + +S+ ATMLL T+EE AFVLADNLL+ V TD

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Sbjct: 611 KAIVDTVDNLLRAETLDCWKHMNSSEQAHTATMLLDTLEEGAFVLADNLLLEPTRVSMPTD 670

Query: 108 NIKLEVARLSTEG 120

NI LEVA LSTEG

Sbjct: 671 NIVLEVAVLSTEG 683

☐ >gi|7513944|pir|T17160 CL2BA protein - rat
 gi|3695129|gb|AAC62657.1| CL2BA [Rattus norvegicus]
 Length = 1467

Score = 106 bits (264), Expect = 6e-23

Identities = 61/133 (45%), Positives = 78/133 (58%), Gaps = 13/133 (9%)

Query: 1 AENTRNHLNAGDITYSVRAMDNLVGLLDVNLRLNTPGGKDSAARSLN----- 47

A++T+ + AGD++ SVR M+ LV +LD L+ L P KDSA RS N

Sbjct: 551 AKHTKGTVFAGDVSSSVRLMEQLVDILDAQLQELKPSEKDSAGRSYNKLQKREKTCRAYL 610

Query: 48 KAMVETVXXXXXXXXXXXXWRDLTTSNLRRAATMLLHTVEESAFVLADNLLKTDIVRENTD 107

KA+V+TV W+ + +S+ ATMLL T+EE AFVLADNLL+ V TD

Sbjct: 611 KAIVDTVDNLLRAETLDCWKHMNSSEQAHTATMLLDTLEEGAFVLADNLLLEPTRVSMPTD 670

Query: 108 NIKLEVARLSTEG 120

NI LEVA LSTEG

Sbjct: 671 NIVLEVAVLSTEG 683

☐ >gi|7513943|pir|T17159 CL2AC protein - rat
 gi|3695127|gb|AAC62656.1| CL2AC [Rattus norvegicus]
 Length = 1463

Score = 106 bits (264), Expect = 6e-23

Identities = 61/133 (45%), Positives = 78/133 (58%), Gaps = 13/133 (9%)

Query: 1 AENTRNHLNAGDITYSVRAMDNLVGLLDVNLRLNTPGGKDSAARSLN----- 47

A++T+ + AGD++ SVR M+ LV +LD L+ L P KDSA RS N

Sbjct: 551 AKHTKGTVFAGDVSSSVRLMEQLVDILDAQLQELKPSEKDSAGRSYNKLQKREKTCRAYL 610

Query: 48 KAMVETVXXXXXXXXXXXXWRDLTTSNLRRAATMLLHTVEESAFVLADNLLKTDIVRENTD 107

KA+V+TV W+ + +S+ ATMLL T+EE AFVLADNLL+ V TD

Sbjct: 611 KAIVDTVDNLLRAETLDCWKHMNSSEQAHTATMLLDTLEEGAFVLADNLLLEPTRVSMPTD 670

Query: 108 NIKLEVARLSTEG 120

NI LEVA LSTEG

Sbjct: 671 NIVLEVAVLSTEG 683

☐ >gi|19705539|ref|NP_599235.1| calcium-independent alpha-latrotoxin receptor hom
 norvegicus]
 gi|7513907|pir|T14324 alpha-latrotoxin receptor, calcium-independent - rat
 gi|3766205|gb|AAC77815.1| calcium-independent alpha-latrotoxin receptor homolog
 norvegicus]
 Length = 1487

Score = 106 bits (264), Expect = 7e-23

Identities = 61/133 (45%), Positives = 78/133 (58%), Gaps = 13/133 (9%)

Query: 1 AENTRNHLNAGDITYSVRAMDNLVGLLDVNLRLNTPGGKDSAARSLN----- 47

A++T+ + AGD++ SVR M+ LV +LD L+ L P KDSA RS N

Sbjct: 551 AKHTKGTVFAGDVSSSVRLMEQLVDILDAQLQELKPSEKDSAGRSYNKLQKREKTCRAYL 610

Query: 48 KAMVETVXXXXXXXXXXXXWRDLTTSNLRRAATMLLHTVEESAFVLADNLLKTDIVRENTD 107

KA+V+TV W+ + +S+ ATMLL T+EE AFVLADNLL+ V TD

Sbjct: 611 KAIVDTVDNLLRAETLDCWKHMNSSEQAHTATMLLDTLEEGAFVLADNLLLEPTRVSMPTD 670

Query: 108 NIKLEVARLSTEG 120

NI LEVA LSTEG

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Sbjct: 671 NIVLEVAVLSTEG 683

☐ >gi|7513945|pir|T17185 CL2BC protein - rat
gi|3695133|gb|AAC62659.1| CL2BC [Rattus norvegicus]
Length = 1478

Score = 106 bits (264), Expect = 7e-23
Identities = 61/133 (45%), Positives = 78/133 (58%), Gaps = 13/133 (9%)

Query: 1 AENTRNHLNAGDITYSVRAMDNLVGLLDVNLRLNLTGGKDSAARSLN----- 47
A++T+ + AGD++ SVR M+ LV +LD L+ L P KDSA RS N
Sbjct: 551 AKHTKGTVFAGDVSSSVRLMEQLVDILDAQLQELKPSEKDSAGRSYNKLQKREKTCRAYL 610
Query: 48 KAMVETVXXXXXXXXXXXXWRDLTTSNLRRAATMLLHTVEESAFVLADNLLKTDIVRENTD 107
KA+V+TV W+ + +S+ ATMLL T+EE AFVLADNLL+ V TD
Sbjct: 611 KAIVDTVDNLLRAETLDCWKHMNSSEQAHTATMLLDTLEEGAFVLADNLLLEPTRVSMPTD 670
Query: 108 NIKLEVARLSTEG 120
NI LEVA LSTEG
Sbjct: 671 NIVLEVAVLSTEG 683

☐ >gi|3882293|dbj|BAA34506.1| KIAA0786 protein [Homo sapiens]
Length = 1021

Score = 103 bits (257), Expect = 4e-22
Identities = 60/133 (45%), Positives = 78/133 (58%), Gaps = 13/133 (9%)

Query: 1 AENTRNHLNAGDITYSVRAMDNLVGLLDVNLRLNLTGGKDSAARSLN----- 47
A++T+ + AGD++ SVR M+ LV +LD L+ L P KDSA RS N
Sbjct: 109 AKHTKGPVFAGDVSSSVRLMEQLVDILDAQLQELKPSEKDSAGRSYNKLQKREKTCRAYL 168
Query: 48 KAMVETVXXXXXXXXXXXXWRDLTTSNLRRAATMLLHTVEESAFVLADNLLKTDIVRENTD 107
KA+V+TV W+ + +S+ ATMLL T+EE AFVLADNLL+ V T+
Sbjct: 169 KAIVDTVDNLLRPEALESWKHMNSSEQAHTATMLLDTLEEGAFVLADNLLLEPTRVSMPTD 228
Query: 108 NIKLEVARLSTEG 120
NI LEVA LSTEG
Sbjct: 229 NIVLEVAVLSTEG 241

☐ >gi|7513494|pir|T18385 latrophilin-2 (splice variant bbbae) - bovine
gi|4164045|gb|AAD05317.1| latrophilin 2 splice variant bbbae [Bos taurus]
Length = 1420

Score = 103 bits (256), Expect = 5e-22
Identities = 59/133 (44%), Positives = 78/133 (58%), Gaps = 13/133 (9%)

Query: 1 AENTRNHLNAGDITYSVRAMDNLVGLLDVNLRLNLTGGKDSAARSLN----- 47
A++T+ + AGD++ SVR M+ LV +LD L+ L P KDSA RS N
Sbjct: 551 AKHTKGPVFAGDVSSSVRLMEQLVDILDAQLQELKPSEKDSAGRSYNKLQKREKTCRAYL 610
Query: 48 KAMVETVXXXXXXXXXXXXWRDLTTSNLRRAATMLLHTVEESAFVLADNLLKTDIVRENTD 107
KA+V+TV W+ + +S+ ATMLL T+EE AFVLADNL++ V T+
Sbjct: 611 KAIVDTVDNLLRPEALESWKHMNSSEQAHTATMLLDTLEEGAFVLADNLVEPTRVSMPTD 670
Query: 108 NIKLEVARLSTEG 120
NI LEVA LSTEG
Sbjct: 671 NIVLEVAVLSTEG 683

☐ >gi|7513496|pir|T18387 latrophilin-2 (splice variant bbbbe) - bovine
gi|4164049|gb|AAD05319.1| latrophilin 2 splice variant bbbbe [Bos taurus]
Length = 1435

Score = 103 bits (256), Expect = 5e-22
Identities = 59/133 (44%), Positives = 78/133 (58%), Gaps = 13/133 (9%)

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Query: 1 AENTRNHLNAGDITYSVRAMDNLVGLLDVNLRLNLTTPGGKDSAARSLN----- 47
 A++T+ + AGD++ SVR M+ LV +LD L+ L P KDSA RS N
 Sbjct: 551 AKHTKGPVFAGDVSSSVRLMEQLVDILDAQLQELKPSEKDSAGRSYNKLQKREKTCRAYL 610

Query: 48 KAMVETVXXXXXXXXXXXXWRDLTTSNLRRAATMLLHTVEESAFVLADNLLKTDIVRENTD 107
 KA+V+TV W+ + +S+ ATMLL T+EE AFVLADNL++ V T+
 Sbjct: 611 KAIVDTVDNLLRPEALESWKHMNSSEQAHTATMLLDTLEEGAFVLADNLVEPTRVSMPT 670

Query: 108 NIKLEVARLSTEG 120
 NI LEVA LSTEG
 Sbjct: 671 NIVLEVAVLSTEG 683

☐ >gi|7513487|pir||T18375 latrophilin-2 (splice variant babae) - bovine
 gi|4164029|gb|AAD05309.1| latrophilin 2 splice variant babae [Bos taurus]
 Length = 1354

Score = 103 bits (256), Expect = 5e-22
 Identities = 59/133 (44%), Positives = 78/133 (58%), Gaps = 13/133 (9%)

Query: 1 AENTRNHLNAGDITYSVRAMDNLVGLLDVNLRLNLTTPGGKDSAARSLN----- 47
 A++T+ + AGD++ SVR M+ LV +LD L+ L P KDSA RS N
 Sbjct: 485 AKHTKGPVFAGDVSSSVRLMEQLVDILDAQLQELKPSEKDSAGRSYNKLQKREKTCRAYL 544

Query: 48 KAMVETVXXXXXXXXXXXXWRDLTTSNLRRAATMLLHTVEESAFVLADNLLKTDIVRENTD 107
 KA+V+TV W+ + +S+ ATMLL T+EE AFVLADNL++ V T+
 Sbjct: 545 KAIVDTVDNLLRPEALESWKHMNSSEQAHTATMLLDTLEEGAFVLADNLVEPTRVSMPT 604

Query: 108 NIKLEVARLSTEG 120
 NI LEVA LSTEG
 Sbjct: 605 NIVLEVAVLSTEG 617

☐ >gi|7513489|pir||T18379 latrophilin-2 (splice variant babbe) - bovine
 gi|4164033|gb|AAD05311.1| latrophilin 2 splice variant babbe [Bos taurus]
 Length = 1369

Score = 103 bits (256), Expect = 6e-22
 Identities = 59/133 (44%), Positives = 78/133 (58%), Gaps = 13/133 (9%)

Query: 1 AENTRNHLNAGDITYSVRAMDNLVGLLDVNLRLNLTTPGGKDSAARSLN----- 47
 A++T+ + AGD++ SVR M+ LV +LD L+ L P KDSA RS N
 Sbjct: 485 AKHTKGPVFAGDVSSSVRLMEQLVDILDAQLQELKPSEKDSAGRSYNKLQKREKTCRAYL 544

Query: 48 KAMVETVXXXXXXXXXXXXWRDLTTSNLRRAATMLLHTVEESAFVLADNLLKTDIVRENTD 107
 KA+V+TV W+ + +S+ ATMLL T+EE AFVLADNL++ V T+
 Sbjct: 545 KAIVDTVDNLLRPEALESWKHMNSSEQAHTATMLLDTLEEGAFVLADNLVEPTRVSMPT 604

Query: 108 NIKLEVARLSTEG 120
 NI LEVA LSTEG
 Sbjct: 605 NIVLEVAVLSTEG 617

☐ >gi|7513495|pir||T18386 latrophilin-2 (splice variant bbbaf) - bovine
 gi|4164047|gb|AAD05318.1| latrophilin 2 splice variant bbbaf [Bos taurus]
 Length = 1463

Score = 103 bits (256), Expect = 6e-22
 Identities = 59/133 (44%), Positives = 78/133 (58%), Gaps = 13/133 (9%)

Query: 1 AENTRNHLNAGDITYSVRAMDNLVGLLDVNLRLNLTTPGGKDSAARSLN----- 47
 A++T+ + AGD++ SVR M+ LV +LD L+ L P KDSA RS N
 Sbjct: 551 AKHTKGPVFAGDVSSSVRLMEQLVDILDAQLQELKPSEKDSAGRSYNKLQKREKTCRAYL 610

Query: 48 KAMVETVXXXXXXXXXXXXWRDLTTSNLRRAATMLLHTVEESAFVLADNLLKTDIVRENTD 107
 KA+V+TV W+ + +S+ ATMLL T+EE AFVLADNL++ V T+
 Sbjct: 611 KAIVDTVDNLLRPEALESWKHMNSSEQAHTATMLLDTLEEGAFVLADNLVEPTRVSMPT 670

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